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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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1 RGDLMFLLDSSASVSHYEFS......FVDVDDLHIIVQELRGSILD 180
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

QY 123 PMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGSI 178	Matches 61; Conservative 33; Mismatches 82; Indels 1; Gaps 1; Qy 3 DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS 62 :-	alternative splicing; in: signal sequence #st roduct: collagen alpha main: fibronectin type omain: fib	RESULT 1 \$31212 collagen alpha 1(XIV) chain precursor, short form - chicken C;Species: Gallus gallus (chicken) C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003 C;Accession: S31212 R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B. Bur: J. Biochem. 212, 483-490, 1993 A;Title: Complete primary structure of chicken collagen XIV. A;Reference number: S31211; MVID:93185668; PMID:8444186 A;Accession: S31212 A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: mRNA A;Residues: 1-1857 <wae> A;Cross-references: UNIPARC:UPI000017123C; EMBL:X70792; NID:9288874; PIDN:CAA50063.1; PI A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993 C;Genetics:</wae>

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C;Keywords: alternative splicing; coiled coil; extracellular ma F;1-28/Domain: signal sequence #status predicted <SIG> F;29-188B/Product: collagen alpha 1(XIV) chain, long form #stat: F;29-110/Domain: fibronectin type III repeat homology <FN3A> F;29-110/Domain: von Willebrand factor type A repeat homology <FN3B> F;156-320/Domain: fibronectin type III repeat homology <FN3B> F;352-433/Domain: fibronectin type III repeat homology <FN3B> F;442-525/Domain: fibronectin type III repeat homology <FN3D> F;534-614/Domain: fibronectin type III repeat homology <FN3D> F;534-614/Domain: fibronectin type III repeat homology <FN3B> F;623-707/Domain: fibronectin type III repeat homology <FN3B> F;632-94/Domain: fibronectin type III repeat homology <FN3G> F;922-1009/Domain: fibronectin type III
A;Cross-references: UNIPROT:P13944; UNIPARC:UPI0000126D2D; GB:D00824; NID:g222810; A;Note: in the authors' translation residues 1216-1219 are shown after residue 1231 R;Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R. J. Biol. Chem. 264, 19772-19778, 1989
A;Title: Type XII collagen. A large multidomain molecule with partial homology to A;Reference number: A34485; MUID:90062079; PMID:2584192
                                                                                                                                                                                                                                                                                                                       J. Cell Biol. 115, 209-221, 1991
A;Title: The complete primary structure of type XII collagen shows a chimeric molecule nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp sit A:Reference number: A40020; MUID:92011862; PMID:1918137
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A;Cross-references: UNIPROT:P32018; UNIPARC:UPI0000126D31; EMBL:X70793; A;Cross-references: UNIPROT:P32018; UNIPARC:UPI0000126D31; EMBL:X70793; R;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B. Eur. J. Biochem. 212, 483-490, 1993
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A;Residues: 1-416;1460-1811,1843-1888 <WAE>
A;Cross-references: UNIPARC:UPI00001773F4; C;Genetics:
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;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
;Accession: S78476; S31211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004;Accession: A40020; A34485; B34485; A28037; S23814; S22254; S28811; Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Species: Gallus gallus (chicken)
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15, 209-221, 19
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       F;2028-2110/Domain:
F;2119-2199/Domain:
F;2207-2294/Domain:
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F;1384-1465/Domain:
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F;332-414/Domain: fibronectin type III repeat homology <FN3B>
F;437-601/Domain: von Willebrand factor type A repeat homology <
F;629-1178/Domain: IIIC #status predicted <IIC>
F;630-711/Domain: fibronectin type III repeat homology <FN3C>
F;721-802/Domain: fibronectin type III repeat homology <FN3D>
F;812-895/Domain: fibronectin type III repeat homology <FN3E>
F;812-895/Domain: fibronectin type III repeat homology <FN3F>
F;905-986/Domain: fibronectin type III repeat homology <FN3F>
F;905-986/Domain: fibronectin type III repeat homology <FN3H>
F;1086-1169/Domain: fibronectin type III repeat homology <FN3H>
F;1197-1361/Domain: von Willebrand factor type A repeat homology
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F;24-105/Domain: fibronectin type III repeat homology <FN3A>
F;137-301/Domain: von Willebrand factor type A repeat homolog
F;137-425/Domain: IIIB #status predicted <IIIB>
F:332-425/Domain: IIIB #status predicted <IIIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Introns: 2845/3; 2863/3; 2887/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1 C;Keywords: alternative splicing; cell binding; coiled coil; connective t F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-3124/Product: collagen alpha 1(XII) chain #status predicted <MAT>
F;24,1189-3124/Product: collagen alpha 1(XII) chain short splice form #st
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Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A;Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA
A;Reference number: A28037; MUID:87317590; PMID:3476925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 2831-2832,'T',2834,'R',2836-2843;3002-3014 <DUB>
A;Cross-references: UNIPARC:UPI0000173C44; UNIPARC:UPI0000173C45
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J. Biol. Chem. 262, 1724-17727, 1987
A;Tille: Type XII collagen is expressed in embryonic chick tendons. Isolation A;Reference number: S22254; MUID:88087065; PMID:3121603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Biochem. 207, 847-856, 1992
A;Title: A major oligomeric fibroblast proteoglycan identified
A;Reference number: S23814; MUID:92362621; PMID:1323460
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A;Note: this sequence has been revised in
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A;Residues: 2456-2758,'A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A;Cross-references: UNIPARC:UPI0000171233; EMBL:J05137; NID:g211284; PIDN:AAA48635.1;
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A;Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280 <TRU>
A;Cross_references: UNIPARC:UPI0000173C46; EMBL:X67327
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A;Title: The two splice variants of collagen XII share a common
A;Reference number: S28811; MUID:93042014; PMID:1420368
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A;Residues: 2772-2792;2846-2873 <GOR2>
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                                  repeat
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Eur. J. Biochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MUID:92339443; PMID:1339349
A;Accession: S22916
                                                                                                                                                                  R;Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, Eur. J. Biochem. 201, 333-338, 1991
A;Title: Cloning of a cDNA for a new member of the class A;Reference number: S17035; MUID:92037585; PMID:1935930
                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 286-494, 'Q', 496-834, 'A', 836-1119, 'KL', 1122-1402, 1409-1439
A; Cross references: UNIPARC: UPI0000173C48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P32018; UNIPARC:UPI0000173C47
A;Experimental source: embryo skin
A;Note: sequence inconsistent with the nucleotide transla
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                                                              A; Residues: 1472-1659 < GOR1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1472-1660 < APT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, March 1992 A; Reference number: S30085
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                                                                                                A; Molecule type: mRNA
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F;2438-2440/Region: c
F;2509-2750/Domain: I
F;2751-2902/Domain: c
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Matches 62
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;2903-2945/Domain:
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Cross-references: UNIPARC: UPI0000173C49 Accession: S20833
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38-2440/Region: cell adhesion #status predicted
09-2750/Domain: IXP, homologous to NC4 domain of type IX collagen #status
51-2902/Domain: collagenous COL2 #status predicted <COL2>
99-2901/Region: cell attachment (R-G-D) motif
03-2945/Domain: non-collagenous NC2 #status predicted <NC2>
46-3048/Domain: non-collagenous NC1 #status predicted <COL1>
49-3124/Domain: non-collagenous NC1 #status predicted <NC1>
49-3124/Domain: non-collagenous NC1 #status predicted <NC1>
(R-G-D) motif
03-2945/Domain: non-collagenous NC2 #status predicted <NC1>
(R-G-D) motified site: carbohydrate (R-G-D) motified site: hydroxyproline (R-G-D) motified site: hydroxypro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from NCBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoded by alternative transcripts
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f
                                                                                                                                                                                                                                                                      T.F.; van
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GEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPVGP : | | : | : | : | : | | | | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

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R;Kiss, I.; Deak, F.; Holloway Jr., R.G.; Delius, H.; Mebust, K. J. Biol. Chem. 264, 8126-8134, 1989
A,Title: Structure of the gene for cartilage matrix protein, a grins, Von Willebrand factor, complement factors B and C2, and A,Reference number: A33809; MUID:89255246; PMID:2542265
A;Accession: A33809
                                                                                                                                                                                                                                                                        C;Superfamily: cartilage matrix protein; EGF homology F;37-204/Domain: von Willebrand factor type A repeat F;225-260/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                           A;Accession: A26364
A;Molecule type: mRNA
A;Residues: 78-493 <ARG>
A;Cross-references: UNIPARC:UPI000004F1EE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P05099; UNIPARC:UPI000004F1EF; GB:X12346; GB:X12347; R;Argraves, W.S.; Deak, F.; Sparks, K.J.; Kiss, I.; Goetinck, P.F. Proc. Natl. Acad. Sci. U.S.A. 84, 464-468, 1987
A;Title: Structural features of cartilage matrix protein deduced from cDNA.
A;Reference number: A26364; MUID:87092429; PMID:3025875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cartilage matrix protein precursor - chicken
c;Species: Gallus gallus (chicken)
c;Species: Gallus gallus (chicken)
C;Date: 09-Mar-1990 #sequence revision 09-Mar-1990 #text_change 09-Jul-2004
C;Accession: A33809; A26364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;40-204/Domain: von Willebrand factor type A repeat homology <VWA1>
F;336-317/Domain: fibronectin type III repeat homology <FW3A>
F;326-409/Domain: fibronectin type III repeat homology <FW3B>
F;418-498/Domain: fibronectin type III repeat homology <FW3C>
F;507-591/Domain: fibronectin type III repeat homology <FW3D>
F;625-707/Domain: fibronectin type III repeat homology <FW3D>
F;625-707/Domain: fibronectin type III repeat homology <FW3D>
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A;Residues: 1551-1570;1593-1599;1639-1667 <GOR2>
A;Cross-references: UNIPARC:UPI0000173C49
A;Cross-seferences: Uniparcial colled coll; extracellular matrix; glycoprotein; trime C;Keywords: alternative splicing; colled coll; extracellular matrix; glycoprotein; trime F;40-204/Domain: von Willebrand factor type A repeat homology <VWA1>
F;236-317/Domain: fibronectin type III repeat homology <PW3A>
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                                                   S
                                                                                                                                                                                                                                       F;225-260/Domain: EGF homology <EGF>
F;270-434/Domain: von Willebrand factor type A repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-493 <KIS>
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DLVFLIDGSKSVRPENFELVKKFINQIVESLEVSEKQAQVGLVQYSSSVRQEFPLGQFKN
                                                         DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDAVLDADRNLPYKGGNTLTGLALTYILENCFKPEAGARPGVSKIGILITDGKSQDDVIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                27.1%; Score 247.5; 38.0%; Pred. No. 2e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
                                                                                                       Pred. No. 20
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Pred. No. 2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                     E; GB:M14792; NID:g211545; PIDN:AAA48695.1; EGF homology; von Willebrand factor type A
                                                                                                                                                       2e-14;
                                                                                                                                                                             DB 2;
                                                                                                                          78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83;
                                                                                                                                                                                                                                                                                                        homology <VWA1>
                                                                                                                                                                                                                                           homology <VWA2>
                                                                                                                                                                                 Length
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A;Map position: 1p35-1p35
A;Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1 C;Complex: homotrimer
C;Superfamily: cartilage matrix protein; EGF homology; vor
                                                                                                                                                                                                                                                                                                                                                                                                                                            cartilage matrix protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Uul-1991 #sequence_revision 12-Jul-1991 #text_change 09-Jul-2004
C;Accession: A37979; B37979
C;Accession: A37979; B37979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
A37979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 r;30-500/Product: cartilage matrix protein #status predicted <MAT>F;43-210/Domain: von Willebrand factor type A repeat homology <VWAF;231-266/Domain: EGF homology <PGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cartilage matrix protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
                                                                                                                     A;Gene: GDB:CRTM
                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 157-290, 'L', 292-496 <JE2>
A; Cross-references: UNIPARC: UPI000016A6E8;
                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P21941; UNIPARC:UPI000004F1ED; A;Accession: B37979
                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-496 < JEN>
                                                                                                                                                                                                                                                                                                                                A; Reference number: A37979; A; Accession: A37979
                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 265, 1902 Tritle: Structure and chromosomal location A; Title: Structure and chromosomal location and mumber: A37979; MUID:91060568;
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A; Residues: 1-500 < ASZ>
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                                                                                             A; Cross-references:
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                                                                                                                                                Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRDVSERARASGIELFAIGLGRVDKATLRQIASEPQDEHVDYVE 208
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                                                                                               GDB:127280;
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34.8%; Pred. No. 1e-1
tive 29; Mismatches
                                                                                               OMIM:115437
                                                                                                                                                                                                                                                                                                                                                                                                                              S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers,
                                                                                                                                                                                                                                                                                                                                                                               location of the human gene encoding cartilage matrix
                                                                                                                                                                                                                                                                                                                                                              PMID:2246248
                                                                                                                                                                    GB:M55683;
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    Willebrand
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  type
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    J. Biol.
A;Title:
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C;Keywords: glycoprotein; homotrimer
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-496/Product: cartilage matrix protein #status predicted <WAT>
F;39-206/Domain: von Willebrand factor type A repeat homology <VWA
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F;273-437/Domain: von Willebrand factor type A repeat homology <VWA2>
F;76,344/Binding site: carbohydrate (Asn) (covalent) #status predicter
F;76,344-816-1348,234-247,249-262/Disulfide bonds: #status predicted
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395
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                                                                                                                                   63 GEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPVGP 122
                                                                                                                                                                                                                              3 DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS 62
                                                                                                                                                                                                                                                                         l Similarity
62; Conserv
AAKKAKDLGFKMFAVGVGNAVEDELREIASEPVAEHYFYTADFKTINQIGKKLQKKI
                                                                                                                                                                                   DLVFLIDGSKSVRPENFELVKKFISQIVDTLDVSDKLAQVGLVQYSSSVRQEFPLGRFHT 334
                                          PMQELKDLGVTVFIVSTGRGNFLELSAAASAP-AEKHLHFVDVDDLHIIVQELRGSI 178
                                                                                             KKDIKAAVRNMSYMEKGTMTGAALKYLIDNSFTVSSGARPGAQKVGIVFTDGRSQDYIND 394
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35.0%;
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Pred. No. 3.5e-13;
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  451
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C;Date: 04-Nov-1994 #Bequence revision 04-Nov-1994 #text change 09-Jul-2004 C;Accession: A54849; PH0844; \$\overline{S}16316; I56328; A30296; I84\overline{6}86 R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J. J. Biol. Chem. 269, 20256-20262, 1994 A;Title: Cloning of human type VII collagen. Complete primary sequence of the A;Reference number: A54849; MUID:94327588; PMID:8051117 A;Accession: A54849 collagen alpha 1(VII) chain precursor - human N,Alternate names: procollagen alpha 1(VII) chain C;Species: Homo sapiens (man) C;Date: 04-Nov-1994 #sequence revision 04-Nov-1994 A; Molecule type: mRNA A; Residues: 1-2944 < CHR > A; Status: not compared with conceptual translation A54849 œ the alpha1(VII)

R;Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S. Biochem. Biophys. Res. Commun. 183, 958-963, 1992 A;Title: Molecular cloning and characterization of type A;Reference number: PH0844; MUID:92231902; PMID:1567409 A; Cross-references: UNIPROT: Q02388; UNIPARC: UPI000017A138; VII collagen GB:L02870; NID:g987124; PIDN:

A; Accession: PH0844

A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Cross-references: UNIPARC: UPI000017A139; DDBJ:D1152; DDBJ:D13694; NID:g453698; PIDN:l
A;Cross-reference translated the codon ACC for residues 394 and 397 as Tyr
R;Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, E.A.; Mar
R;Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, E.A.; Mar
Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A;Fitle: Human type VII collagen: cDNA cloning and chromosomal mapping of the gene.
A;Reference number: S16316; MUID:91334380; PMID:1871109 Mat ₽,

A; Molecule type: mRNA A; Residues: 'EFR', 372-517, 'DV', 520-540, 'W', 542-1255 < RES> A; Cross-references: UNIPARC: UPI000016B3AC; GB: S51236; NID. A; Cross-references: UNIPARC: UPI000016B3AC; GB: S51236; NID. R; Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; C J. Biol. Chem. 264, 3822-3826, 1989 A;Experimental source: keratinocyte R;Gammon, W.R.; Abernethy, M.L.; Padilla, K.M.; Prisayanh, P.S.; Cook, M.E. J. Invest. Dermatol. 99, 691-696, 1992 A;Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain A;Status: translated from GB/EMBL/DDBJ A; Reference number: 156328; MUID:93107742; A; Accession: 156328 A;Molecule type: mRNA A;Residues: 815-892,'E',894-1439 <PAR> A;Cross-references: UNIPARC:UP1000016A722; GB:M65158; GB:S49017; NID:g180914; PIDN:AAA96 Cook, M.E.; Wright, adhesion

prot J.;

Chem. 264, 3 Cleavage of

collagen

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interstitial collagenase GB:S51236; NID:g262308; Morris, N.P.; Glanville,

and

type IV

collagenas R.E.

PIDN:AAB24637.1; , R.W.; Burgeson,

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F;954-1045/Domain: fibronectin type III repeat homology <FN9>
F;1052-1219/Domain: von willebrand factor type A repeat homology <VWA2>
F;1170-1172/Begion: cell attachment (R-G-D) motif
F;1189-1253/Region: cysteine/proline-rich
F;1254-2783/Region: citerrupted helical
F;1334-1336/Region: cell attachment (R-G-D) motif
F;2008-2010/Region: cell attachment (R-G-D) motif
F;2008-2010/Region: cell attachment (R-G-D) motif
F;2553-2555/Region: cell attachment (R-G-D) motif
F;2573-2555/Region: cell attachment (R-G-D) motif
F;2574-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
F;2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>F;2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>F;337,786,1109/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;2157,2185,2188,2664,2667,2673/Modified site: 4-hydroxyproline (Pro) #s
F;2625,2631/Modified site: 5-hydroxylysine (Lys) #status experimental
F;2625,2631/Binding site: carbohydrate (Lys) (covalent) #status experimental
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A;Residues: 'A',1240-1246,'G',1248-1250,'XE',1253-1255,'Q',1257,'E';2032,'C',2034-2041;'
A;Cross-references: UNIPARC:UPI000017A13A; UNIPARC:UPI000017A13B; UNIPARC:UPI000017A13C;
A:Note: two reported peptides cannot be reliably located
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F;331-318/Domain: fibronectin type III repeat homology <FW1>
F;327-413/Domain: fibronectin type III repeat homology <FW2>
F;327-413/Domain: fibronectin type III repeat homology <FW2>
F;414-502/Domain: fibronectin type III repeat homology <FW3>
F;508-593/Domain: fibronectin type III repeat homology <FW4>
F;598-683/Domain: fibronectin type III repeat homology <FW9>
F;686-771/Domain: fibronectin type III repeat homology <FW9>
F;686-791/Domain: fibronectin type III repeat homology <FW9>
F;864-952/Domain: fibrone
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F;17-2944/Product: collagen alpha 1(VII) chain #status predicted <MAT>
F;17-1253/Domain: amino-terminal nonhelical #status predicted <NCI>
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A;Note: defects in this gene can result in dominant and recessive dystrophic epidermolys
A;Note: there are 118 introns
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A;Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly --> Ser sub; A;Reference number: A55255; MUID:94224777; PMID:8170945
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A;Title: The carboxyl-terminal half of type VII collagen, A;Reference number: I48103; MUID:93271985; PMID:8499916
A;Accession: I84686
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A; Residues: 2395-2871, 'S', 2873-2944 < RE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
      121
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                                                                                                                          98 GSGGDVIRAIRELSYKGGNTRTGAAILHVADHVFLPQL-ARPGVPKVCILITDGKSQDLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,2804/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 DLMFLIDSSASVSHYEFSRVREFVGQLVAPLPLGTGA--LRASLVHVGSRPYTEFPFGQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
      GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVD 163
                                                                                                                                                                                                                                        SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
                                                                                                                                                                                                                                                                                                                                                      DIVFLLDGSSSIGRSNFREVRSFLEGLVLPFSGAASAQGVRFATVQYSDDPRTEFGLDAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Mismatches
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밁
157 DTAAQRLKGQGVKLFAVGIKNADPEELKRVASQPTSDFFFFVN
 199
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F;239-404/Domain: von Willebrand factor type A repeat homology < VW02>
F;442-607/Domain: von Willebrand factor type A repeat homology < VW03>
F;442-607/Domain: von Willebrand factor type A repeat homology < VW04>
F;840-1004/Domain: von Willebrand factor type A repeat homology < VW04>
F;1033-1197/Domain: von Willebrand factor type A repeat homology < VW05>
F;1039-1400/Domain: von Willebrand factor type A repeat homology < VW07>
F;1439-1604/Domain: von Willebrand factor type A repeat homology < VW08>
F;1639-1804/Domain: von Willebrand factor type A repeat homology < VW08>
F;1639-1804/Domain: von Willebrand factor type A repeat homology < VW09>
F;1838-2010/Domain: von Willebrand factor type A repeat homology < VW10>
F;2043-2378/Domain: collagenous #status predicted <COL>
F;2045-2047/Region: cell attachment (R-G-D) motif
F;2153-2155/Region: cell attachment (R-G-D) motif
F;2159-2151/Region: cell attachment (R-G-D) motif
F;2169-2577/Domain: non-collagenous #status predicted <CNC>
F;2633-2806/Domain: non-collagenous #status predicted <CNC>
F;2633-2806/Domain: von Willebrand factor type A repeat homology < VW12>
F;2633-2806/Domain: platelet glycoprotein Ib-like #status predicted <GPI>
F;2893-3039/Domain: platelet glycoprotein Ib-like #status predicted <GPI>
F;201,2084,2436,2563,2581,2683,2867,2920,3003/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Bonaldo, P.; Russo, V.; Bucciotti, F.; Doliana, R.; Colombatti, A. Biochemistry 29, 1245-1254, 1990
A;Title: Structural and functional features of the alpha3 chain indicate A;Reference number: A34270; MUID:90212613; PMID:2322559
A;Accession: A34270
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J. Cell Biol. 111, 2197-2205, 1990 A;Title: Multiple forms of chicken alpha3(VI) collagen chain A;Reference number: A37797; MUID:91035630; PMID:1977751 A;Accession: A37797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
A37797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Keywords: alternative splicing; cell binding; coiled coil; connecti F;1-25/Domain: signal sequence #status predicted <SIG> F;26-3137/Product: collagen alpha 3(VI) chain #status predicted <MAT> F;26-3042/Domain: non-collagenous #status predicted <NNC> F;36-2042/Domain: von Willebrand factor type A repeat homology <VW01> F;36-202/Domain: von Willebrand factor type A repeat homology <VW01>
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J. Biol. Chem. 264, 20235-20239, 1989

A;Title: The carboxyl terminus of the chicken alpha3 chain

A;Reference number: A32674; MUID:90062147; PMID:2584214

A;Accession: A32674
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A;Residues: 1-253;312-321;434-453;504-518;635-655;704-717;832-853 <DOL>
A;Cross-references: UNIPROT:P15989; UNIPARC:UP10000173C31; UNIPARC:UP10000173C32; UNIPAR
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A; Residues: 2151-2199; 2792-3137 < BO2>
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38
                                                                                                                                                                                    Similarity
                                                                      DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS
DIIFLVDSSWSIGKEHFQLVREFLYDVVKALDVGGNDFRFALVQFSGNPHTEFQLNTYPS
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                                                                                                                                                                                23.7%;
                                                                                                                                             Score 216.5; DB
Pred. No. 1e-10;
6; Mismatches
                                                                                                                                                                                                                   DB 2;
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                                                                                                                                             90;
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hypothetical protein DKFZp434J065.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Date: 04-Feb-408
C;Accession: T46488
R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
A;Accession: S13679
A;Molecule type: mRNA
A;Residues: 1-30,237-313,'CWW',318-322,'AR',326-1815,'FD',1818-1819,'ID',1822-3176
A;Cross-references: UNIPARC:UPI0000173C14; EMBL:X52022; NID:g3127925
                                                                               A; Reference number: S13679; A; Accession: S13679
                                                                                                                                                                          A;Residues: 1-3176 <CHU>A;Residues: 1-3176 <CHU>A;Residues: UNIPARC:UPI0000126D4F; A;Cross-references: UNIPROT:P12111; UNIPARC:UPI0000126D4F; R;Chu, M.L.; Zhang, R.Z.; Pan, T.; Stokes, D.; Conway, D.; EMBO J. 9, 385-393, 1990
                                                                                                                                                                                                                                                                                                                     A; Reference number: A59140
A; Accession: A59140
                                                                                                                                                                                                                                                                                                                                                                                               N;Contains: collagen alpha 3(VI) cnain, splice LOIM PATALLY, (C;Species: Homo sapiens (man) C;Species: 21-Nov-1993 #sequence_revision 12-Nov-1999 #text_change 16-Aug-2004 C;Accession: A59140; S13679; S24465; A57083; S28776; S00245; C31952; C29848;
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A; Residues: 1-741 < AAA>
A; Cross-references: UNIPROT: QBNDE6; UNIPARC: UPI000016ACCB; EMBL: AL137638
A; Experimental source: adult testis; clone DKFZp434J065
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A;Accession: T46488
A;Status: preliminary
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                                                                                                                                                      A; Title: Mosaic
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N;Contains: collagen alpha 3(VI) chain,
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                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                              A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                      submitted to GenBank,
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                                                                                                                                   itors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVSEWASKAKANGITMYAVGVGKAIEBELQEIASEPTNKHLFYAEDFSTMDEISEKLKKG
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                                                                                                                                                      structure of
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31.7%;
                                                                                                       MUID:90151612;
                                                                                                                                                    globular domains
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in, splice f
                                                                                                          PMID:1689238
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orm A9/N10(-)
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                                                                                                                                                                                                GB:X52022; NID:g3127925; PIDN Kuo, H.J.; Glanville, R.; May
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A;Molecule type: protein
A;Rolecule type: protein
A;Residues: 574-85;965-973,'X',975-976;1306-1325;1361-1377;1381-1401;1473-1506,'X',1508
A;Residues: 574-85;9618-2037;2374-2410;2445-2459;2466-2469,'X',2471-2474;2504-2508,'X',
A;Cross-references: UNIPARC:UPI0000173C15; UNIPARC:UPI0000173C16; UNIPARC:UPI0000173C17;
C1C; UNIPARC:UPI0000173C1D; UNIPARC:UPI0000173C1E; UNIPARC:UPI0000173C1F; UNIPARC:UPI0000173C2F,
I0000173C25; UNIPARC:UPI0000173C26; UNIPARC:UPI0000173C27
R;Zanussi, S.; Doliana, R.; Segat, D.; Bonaldo, P.; Colombatti, A.
J. Biol. Chem. 267, 24082-24089, 1992
A;Title: The human type VI collagen gene. mRNA and protein variants of the alpha3 chain of A;Reference number: S28776; MUID:93054780; PMID:1339440
A;Reference number: S28776; MUID:93054780; PMID:1339440
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A; Molecule type: DNA A; Residues: 310-328 < ZAN >

A; Accession: S28776 A; Cross-references: UNIPARC: UPI0000173C28

A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Residues: 32-126,'AK',129-136,'L',138-236 <ZA2>
A;Residues: 32-126,'AK',129-136,'L',138-236 <ZA2>
A;Cross-references: UNIPARC:UPI0000173C28; GB:S49432; NID:g260296; PIDN:AAB24261.1;
A;Cross-references: V. Delitzmann, R.; Pribula-Conway, D.; Hsu-Chen, C.C.; Bernard, N R;Chu, M.L.; Mann, K.; Deutzmann, R.; Pribula-Conway, Eur. J. Biochem. 168, 309-317, 1987 Bernard, M.P.;

PID:

A; Title: Characterization of three constituent chains of A; Reference number: S00126; MUID:88029444; PMID:3665927 collagen type VI by peptide seq

A; Accession: S00245

A;Molecule type: mRNA; protein A;Residues: 2024-2046;2092-2156,'R';2203-2208,'X',2210-2211,'X',2213-2227;2228-2251;2314 A;Cross-references: UNIPARC:UP1000016A705; UNIPARC:UP10000173C29; UNIPARC:UP10000173C2A;

A;Note: the mRNA portion of the sequence corresponds to residues 2092-2157 R;Chu, M.L.; Conway, D.; Pan, T.; Baldwin, C.; Mann, K.; Deutzmann, R.; Tin J. Biol. Chem. 263, 18601-18606, 1989 A; Title: Amino acid sequence of the triple-helical domain of human collager A;Reference number: A31952; MUID:89066644; PMID:3198591 A;Accession: C31952 Timpl,

collagen type

A; Molecule type: mRNA A; Residues: 2038-2373 < CH4>

A,Cross-references: UNIPARC:UPI0000173C2E; GB:J04211; GB:M20778 A;Note: parts of this sequence were determined by protein sequencing R;Weil, D.; Mattei, M.G.; Passage, E.; Van Cong, N.; Pribula-Conway, Am. J. Hum. Genet. 42, 435-445, 1988 D.; Mann, K.; Deutzn

A;Title: Cloning and chromosomal localization of human genes A;Reference number: A29848; MUID:88161046; PMID:3348212 A;Accession: C29848 encoding the three chains 0

A; Molecule type: mRNA A; Residues: 2092-2151 <WEI>

A;Cross-references: UNIPARC:UPI000016A720; GB:M27449; NID:g291919; A;Note: part of this sequence was determined by protein sequencing R;Jander, R: Rautenberg, J: Glanville, R.W.

Eur. J. Biochem. 133, 39-46, 1983
A;Title: Further characterization of the three polypeptide chains cap;Reference number: \$26506; MUID:83209648; PMID:6852033 PIDN: AAA52057.1;

PID:

g t

O. bovine and human

A; Accession: S26510

A; Molecule type: protein A; Residues: 'SAIAGVAGVG' < JAN>

A;Cross-references: UNIPARC:UPI0000173C2F
A;Note: this sequence cannot be reliably placed and probably repre
A;Note: this sequence cannot be reliably placed and probably repre
A;Nayer, U.; Poeschl, E.; Nischt, R.; Specks, U.; Pan, T.C.; Chu,
Bur. J. Biochem. 225, 573-580, 1994
A;Title: Recombinant expression and properties of the Kunitz-type
A;Reference number: S48709; MUID:95045506; PMID:7525281 represents the results Chu, M.L.; Timpl, R.

from

protease-inhibitor

A; Accession: S48709

A;Molecule type: mRNA
A;Residues: 'MRAWIFFLLCLAGRALAA',3102-3176
A;Cross-references: UNIPARC:UPI0000173C30 <MAY>

A;Note: engineered sequence to allow isolation of the Kunitz-type proteinase inhibitor R;Arnoux, B.; Merigeau, K.; Saludjian, P.; Norris, F.; Norris, K.; Bjorn, S.; Olsen, O. submitted to the Brookhaven Protein Data Bank, August 1994 ă

A;Contents: annotation; X-ray crystallography, 1.6 angstroms, residues 3106-3160 A;Note: engineered sequence expressed in Saccharomyces cerevisiae strain mt-663 C;Comment: Prolines and lysines at the third position of the tripeptide repeating sines are 5-hydroxylated and subsequently O-glycosylated. C;Comment: The fibronectin type III repeat homology domain may be released during C;Genetics: released during repeating unit

proces

EMBL:U19494; NID:g632647; PII

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reproduct squal sequence #status predicted cSIGs

F126-3176/Product collagen alpha 3(VI) chain #status predicted cANTS
F26-307/Domain: anino-terminal nonhelical #status predicted cANTS
F126-30/Jomain: won Willebrand factor type A repeat homology <WW01>
F126-30/Domain: von Willebrand factor type A repeat homology <WW03>
F126-30/Domain: von Willebrand factor type A repeat homology <WW03>
F126-30/Domain: von Willebrand factor type A repeat homology <WW03>
F126-30/Domain: von Willebrand factor type A repeat homology <WW03>
F126-30/Domain: von Willebrand factor type A repeat homology <WW03>
F127-191/Domain: von Willebrand factor type A repeat homology <WW03>
F127-191/Domain: von Willebrand factor type A repeat homology <WW03>
F127-191/Domain: von Willebrand factor type A repeat homology <WW03>
F127-191/Domain: von Willebrand factor type A repeat homology <WW03>
F127-191/Domain: von Willebrand factor type A repeat homology <WW03>
F128-205/Domain: von Willebrand factor type A repeat homology <WW03>
F128-205/Domain: von Willebrand factor type A repeat homology <WW03>
F128-218/Region: cell attachment (R-G-D) motif
F1216-218/Region: cell attachment (R-G-D) motif
F1216-218/Region: cell attachment (R-G-D) motif
F1217-218/F2100: cell attachment (R-G-D) motif
F1218-219/Domain: von Willebrand factor type A repeat homology <WW11>
F126-219/Comain: von Willebrand factor type A repeat homology <WW11>
F126-219/Comain: von Willebrand factor type A repeat homology <WW11>
F126-219/Comain: von Willebrand factor type A repeat homology <WW11>
F126-219/Comain: von Willebrand factor type A repeat homology <WW11>
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F126-219/Comain: von Willebrand factor type A repeat homology <WW11>
F126-219/Comain: von
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                                                                             A;Reference number: I51027; MUID:95246925; PMID:7729585
A;Accession: I51027
                                                                                                                                                                                                      R; Wei, Y.; Yang, E.V.; K
Dev. Biol. 168, 503-513,
A; Title: Monoclonal anti
                                                                                                                                                                                                                                                                                                                                                                                                       type XII collagen alpha-1 chain - eastern newt (fragment)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
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C;Punction: structural component of extracellular tissue microfibrils associated with C;Superfamily: collagen VI
C;Keywords: alternative splicing; blocked amino end; cell binding; coiled coil; extrace)
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A;Status: preliminary; translated A;Molecule type: mRNA
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Map position: 2937.3-2937.3 (See PIR:CGHUIA); Complex: type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: Type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: Type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: Type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: Type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: Type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: Type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: Type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: Type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: Type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: Type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: Type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: Type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: Type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: Type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: Type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: Type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: Type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: Type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: Type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA); Complex: Type VI collagen is a heterot
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                                                       from GB/EMBL/DDBJ
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J. Biol. Chem. 268, 2989-2996, 1993
A;Title: Expression of native and truncated A;Reference number: A45226; MUID:93155124; FA;Accession: A45226
                                                                                                                                 R; Briesewitz, R.; Epstein, M.R.; Marcantonio,
                                                                                                                                                    C;Accession: A45226
                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994
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A;Molecule type: mRNA
A;Residues: 1-272 <KER>
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A;Title: The role of the I domain in ligand binding of the A;Reference number: A55348; MUID:94357930; PMID:7521332
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A;Residues: 1-929 <WEI>
A;Cross-references: UNIPROT:Q91145; UNIPARC:UPI0000126D2B; EMBL:U1949: F;155-236/Domain: fibronectin type III repeat homology <3FR>
F;631-795/Domain: von Willebrand factor type A repeat homology <VWA3>
A;Status: preliminary;
A;Molecule type: mRNA
                                                                                                                                                                                                                                                      A45226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: A55348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Gallus gallus (chicken)
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                                                                                                                                                                                                                                                                                                                                            LALVTIVEAL 240
                                                                                                                                                                                                                                                                                                                                                                                         --LHIIVQEL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPMQEL----KDLGVTVFIV----STGRGNFL-----ELSAAASAPAEKHLHFVDVDD- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEEVMDAALRIRORGGTOTMTALGIDTAREEAFTEAHGARRGVOKVMVIVTDGESHD--N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEAAQDAVRASAQRMG-DTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 120
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                     not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.7%; Score 198; DB 2; 34.2%; Pred. No. 2.6e-10; rative 26; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.7%;
27.9%;
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Pred. No. 9.9e-10;
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Б.
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A;Cross references: UNIPROT:Q05707; UNIPARC:UDI00000716A9; GB:M64108; NID:g340081; PIDN: C;Keywords: glycoprotein
F;165-246/Domain: fibronectin type III repeat homology <FN3A>
F;255-338/Domain: fibronectin type III repeat homology <FN3B>
F;347-427/Domain: fibronectin type III repeat homology <FN3C>
F;436-520/Domain: fibronectin type III repeat homology <FN3D>
F;436-520/Domain: fibronectin type III repeat homology <FN3F>
F;541-632/Domain: fibronectin type III repeat homology <FN3F>
F;541-733/Domain: fibronectin type III repeat homology <FN3F>
F;731-818/Domain: fibronectin type III repeat homology <FN3F>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         undulin 1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: A40970
R;Just, M.; Herbst, H.; Hummel, M.; Duerkop, H.; Tripier, D.; Stein, H.; Schuppan, D.
J. Biol. Chem. 266, 17326-17332, 1991
A;Title: Undulin is a novel member of the fibronectin-tenascin family of extracellular A;Reference number: A40970; MUID:91373351; PMID:1716629
A;Accession: A40970
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A40970
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A;Cross-references: UNIPROT:P56199; UNIPARC:UPI000012D9EB
A;Experimental source: hepatoblastoma cell line HepG2
A;Note: sequence extracted from NCBI backbone (NCBIP:124326)
F;142-317/Domain: von Willebrand factor type A repeat homology <VWAl>
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Search completed: February 13, 2006, 07:49:17 Job time: 27.7893 secs
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A; Residues: 1-843 < JUS>
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                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                          35 LGTGALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYAKBQLF
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                                                                                                    DSTHVYNVAEFDLMHTVVESL 143
                                                                                                                                                                                                         KPEAGSRTGVSKIGILITDGKSQDDIIPPSRNLRESGVELFAIGVKNADVNELQEIASEP
                                                                                                                                                                                                                                                        AEASGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAP 154
                                                                                                                                                                                                                                                                                                          VGSEKTRIGLAQYSGDPRIEWHLNAFSTKDEVIEAVRNLPYKGGNTLTGLALNYIFENSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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Perfect score:
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Maximum Match 10
Listing first 45
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-MODEL-frame+ n2p.query.fasta 1
-Q2/AbsSWEB spool/US10699035/runat 13022006 062453 25634/app.guery.fasta 1
-DE-Published Applications AA New -OFMT=fastan -SUFFIX=Tabbn -MINNATCH=0.1
-LODPCL=0 -LOODEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=20 -THR SCORE=pct -THR MAX=100
-TRANS=human40.cdi -LIST=45 -DOCALIGN=20 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSTZE=500 -MINLEN=0
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-MODEL=frame+_n2p.model
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.WO RR=US10699035_GCGN 1 1 10_@runat 13022006_062453_25634 -NCPU=6 -ICPU=3

.NO RMAP -NEG SCORES=0 -WAIT -DSPELÖCK=100 -LONGLOG -DEV TIMEOUT=120

.WARN -NEG SCORES=0 -WAIT -LOSPELÖCK=100 -LONGLOG -DEV TIMEOUT=120

.WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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US-11-186-284-26

US-11-190-041-160

US-10-131-826A-294

US-11-113-424-39

US-11-112-449-6

US-11-192-449-5

US-11-192-449-5

US-11-192-449-5

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equence 7, equence 2, equence 4, equence 2,	equence 7, equence 691 equence 688 equence 113 equence 1, equence 921	equence 21, equence 25, equence 6, A equence 4, A equence 3, A equence 338, equence 810,	quence 202, quence 204, quence 206, quence 1802, quence 184, quence 18, quence 24, quence 24, quence 22,	equence 34, A equence 186, equence 186, equence 194, equence 194, equence 198, equence 290,

ALIGNMENTS

RESULT 1 US-10-453-372-2

Sequence 2, Application US/10453372 Publication No. US20060003323A1

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PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/839446
PRIOR APPLICATION NUMBER: 09/839446
PRIOR APPLICATION NUMBER: 09/19476
PRIOR APPLICATION NUMBER: 09/19476
PRIOR APPLICATION NUMBER: 09/983776
PRIOR PILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 60/208263
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 60/208263
PRIOR PILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/227800
PRIOR APPLICATION NUMBER: 60/227800
PRIOR APPLICATION NUMBER: 60/227800
PRIOR APPLICATION NUMBER: 60/227800
PRIOR FILING DATE: 2000-08-25
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APPLICANT: Alsobrook, et al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOL PILE REFERENCE: 21402-589 A
                          Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 1609
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APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
FITLE OF INVENTION: MCYEL GENES, COMPOSITIONS, KITS
FITLE OF INVENTION: MCYELOS FOR IDENTIFICATION, AS:
FILE REFERENCE: MPMO1-029P2RNM
CURRENT APPLICATION UNMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: TO '...'
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                                                                                                                                                                                                                                                                          Sequence 26, Application US/11186284 Publication No. US20050266493A1 GENERAL INFORMATION:
                                                                                                                                                                   APPLICANT: Millennium Pharmaceuticals,
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
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 APPLICATION NUMBER: US/10/301,822 FILING DATE: 2002-11-21
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                                                                                                                                   RESULT 3
US-11-169-041-160
; Sequence 160, Application US/11
; Publication No. US20060019284A1
; GENERAL INFORMATION:
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LENGTH: 3063
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
TITLE OF INVENTION: CELLS
FILE REFERENCE: 10001 NP
CURRENT APPLICATION NUMBER: US/11/169,041
CURRENT FILING DATE: 2005-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
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                                                                                                                                                                                                                                                                           484 ---GACGTGGATGACCTGCACATCATTGTCCAAGAGCTGAGGGGGCTCCATT
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RESULT 4
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PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 527
SOFTWARE: PatentIn version 3.2
SEQ ID NO 160
LENGTH: 517.
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                                         APPLICANT:
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                                                                                              DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
Geritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
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DR FILING DATE: 1997-09-17
DR APPLICATION NUMBER: 60/059263
DR FILING DATE: 1997-09-18
DR APPLICATION NUMBER: 60/059352
DR FILING DATE: 1997-09-19
DR FILING DATE: 1997-09-19
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                                       LeuArgGluAsnValProArgValIleMetIleValThrAspGlyArgProGlnAspSer 176
                                                                                                                                                        GGCCTGGCGCTGGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCA
                                                                                                                                                                                                    LysSerGluValGluArgAlaValLysArgMetArgHisLeuSerThrGlyThrMetThr
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      GTGGGCCCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACC
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                                                                                                                       GlyLeuAlaIleGlnTyrAlaLeuAsnIleAlaPheSerGluAlaGluGlyAlaArgPro
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Watanabe, Colin I
Wood, William
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US-11-113-424-39
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
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Publication No. US20050260713A1
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TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding
FILE REFERENCE: 21402-225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 956
TYPE: PRT
ORGANISM: Homo
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CURRENT FILING DATE: 2005-04-21
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PRIOR FILING DATE: 2001-05-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 190
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FILING DATE: 2000-12-20
APPLICATION NUMBER: 60/311,613
FILING DATE: 2001-08-10
APPLICATION NUMBER: 60/315,617
FILING DATE: 2001-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/256,704 FILING DATE: 2000-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/307,506 FILING DATE: 2001-07-24
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                                                                                     GlyLeuLeuGlnTyrGlySerThrValLysAsnGluPheSerLeuLysThrPheLysArg
                                                                                                                                                         LysGluPheIleValAspIleLeuGlnPheLeuAspIleGlyProAspValThrArgVal
                                                                                                                                                                                                                               AspLeuValPheIleIleAspSerSerArgSerValAsnThrHisAspTyrAlaLysVal
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Best Local Similarity:
Query Match:
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Publication No. US20050281818A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Koteliansky, Victor
TITLE OF INVENTION: Method for the Treatment
FILE REFERENCE: A073-USCN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Biogen, APPLICANT: Gotwal APPLICANT: Koteli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/557,092
PRIOR TILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 60/130,847
PRIOR FILING DATE: 1999-04-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2003-07-22
PRIOR APPLICATION NUMBER: 10/061,658
PRIOR FILING DATE: 2002-02-01
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CURRENT FILING DATE: 2005-07-28
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PRIOR APPLICATION NUMBER: 10/625,260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                      124 AGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACCAGCTCG
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GGTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGT--
                                   GlyIleValGlnTyrGlyGluAsnValThrHisGluPheAsnLeuAsnLysTyrSerSer
                                                                                                       ThrAlaPheLeuAsnAspLeuLeuLysArgMetAspIleGlyProLysGlnThrGlnVal 59
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RESULT 7

US-11-192-449-9

Sequence 9, Application US/11192449

Publication No. US20050281818A1

GENERAL INFORMATION:

APPLICANT: Biogen, Inc.

APPLICANT: Gotwals, Philip

APPLICANT: Gotwals, Philip
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Best Local Similarity:
Query Match:
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PRIOR APPLICATION NUMBER: 10/625,260
PRIOR FILING DATE: 2003-07-22
PRIOR APPLICATION NUMBER: 10/061,658
PRIOR APPLICATION NUMBER: 00/057,092
PRIOR APPLICATION NUMBER: 09/557,092
PRIOR APPLICATION NUMBER: 60/130,847
PRIOR APPLICATION NUMBER: 60/130,847
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 10
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CURRENT FILING DATE: 2005-07-28
                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1999-04-22
APPLICATION NUMBER: 60/137,214
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                                                          AspIleValIleValLeuAspGlySerAsnSerIle-----TyrProTrpAspSerVal
                                                                                                GACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTT
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                                                        Percent Similarity:
Best Local Similari
Query Match:
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US-11-192-449-5
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US-11-192-449-5
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  US-10-699-035A-1 (1-537) x US-11-192-449-5 (1-214)
                                                                                                                                            Pred. No.:
                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/11/192,449
CURRENT FILING DATE: 2005-07-28
PRIOR APPLICATION NUMBER: 10/625,260
PRIOR FILLING DATE: 2003-07-22
PRIOR APPLICATION NUMBER: 10/061,658
PRIOR FILLING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/557,092
PRIOR APPLICATION NUMBER: 09/557,092
PRIOR FILLING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 60/130,847
PRIOR APPLICATION NUMBER: 60/130,847
PRIOR FILLING DATE: 1999-04-22
PRIOR FILLING DATE: 1999-04-22
PRIOR FILLING DATE: 1999-04-22
                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/11192449
Publication No. US20050281818A1
GENERAL INFORMATION:
APPLICANT: Biogen, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gotwals, Philip
APPLICANT: Koteliansky, Victor
TITLE OF INVENTION: Method for the Treatment
FILE REFERENCE: A073-USCN3
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/137,214
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                             LENGTH: 21
TYPE: PRT
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                                                                               Similarity:
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Matches:
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US-10-063-703-34
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  Percent Similarity:
Best Local Similarity:
                                                                              Alignment Scores:
                                                                                                                    ORGANISM: Homo US-10-063-703-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 34, Application US/10063703 Publication No. US20060008901A1 GENERAL INFORMATION:
                                                                                                                                                                                      Prior Application removed -
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3230R1C1
                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/063,703 CURRENT FILING DATE: 2002-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Eaton, Dan L. APPLICANT: Filvaroff, E
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                                                                                                                                                        LENGTH: 67
TYPE: PRT
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Gurney, Austin L.
Watanabe, Colin K.
Wood, William I.
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                      Alignment Scores:
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Publication No.
                                                                                                                    SEQ ID NO 34
LENGTH: 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gurney, Austin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES
TITLE OF INVENTION: ESOPHAGEAL TUMOR
FILE REFERENCE: P3230R1C106C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Goddard, Audrey APPLICANT: Godowski, Paul APPLICANT: Grimaldi, Chri
                                                                                                                                                          PRIOR FILING DATE: 199-12
NUMBER OF SEQ ID NOS: 170
                                                                                                                                                                                                                 PRIOR
                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 10/063662
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 10/006867
PRIOR FILING DATE: 2001-12-06
PRIOR FILING DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/11/102,240 CURRENT FILING DATE: 2005-04-08
                                                                                                                                                                                                                                       PRIOR
                                                                              ORGANISM: Homo
      No.:
                                                                                                                                                                            FILING DATE: 2000-08-24
APPLICATION NUMBER: 60/170262
FILING DATE: 199-12-09
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Grimaldi, Christopher J.
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                       Score:
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TITLE OF INVENTION: DESIRED CONFORMATION AN
FILE REFERENCE: CFBF-P02-021
CURRENT APPLICATION NUMBER: US/11/080,026
CURRENT FILING DATE: 2005-03-15
PRIOR APPLICATION NUMBER: 09/945,265
PRIOR APPLICATION NUMBER: 09/945,265
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,700
PRIOR FILING DATE: 2000-09-01
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Percent Similarity:
                                                                                                    US-11-080-026-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/11080026 Publication No. US20050260192A1 GENERAL INFORMATION:
                                                                                                                                                         NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 4
LENGTH: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Springer, Timothy A. APPLICANT: Shimaoka, Motomu APPLICANT: Lu, Chafen
                                                                                                                     TYPE: PRT
ORGANISM: Homo
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US-10-453-372-186
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                                                    PRIOR APPLICATION NUMBER: 09/78330
PRIOR FILING DATE: 2001-02-23
PRIOR PPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-03-01
PRIOR PPLICATION NUMBER: 60/195792
PRIOR PPLICATION NUMBER: 60/195792
PRIOR PPLICATION NUMBER: 09/839446
PRIOR PPLICATION NUMBER: 09/839446
PRIOR PPLICATION NUMBER: 09/839446
PRIOR PILING DATE: 2000-03-10
PRIOR PILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 09/863776
PRIOR PILING DATE: 2000-03-25
PRIOR PILING DATE: 2000-03-25
PRIOR PILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-23
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  PRIOR PRIOR PRIOR
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CURRENT FILING DATE: 2003-06-03
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APPLICATION NUMBER: 60/208263
FILING DATE: 2000-05-31
APPLICATION NUMBER: 09/939398
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Best Local Similarity:
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              APPLICANT: Alsobrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NU
FILE REFERENCE: 21402-589 A
CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: 09/789390
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2000-03-01
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PRIOR APPLICATION NUMBER: 60/227800
PRIOR FILING DATE: 2000-08-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CURASeqList version 0.1
SEQ ID NO 186
LENGTH: 709
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                      Sequence 180, Application US/10453372 Publication No. US20060003323A1 GENERAL INFORMATION:
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 APPLICATION NUMBER: 09/823187
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PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/19476
PRIOR APPLICATION NUMBER: 60/19476
PRIOR FILING DATE: 2000-03-25
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 09/939398
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LENGTH: 709
 Sequence 194,
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FILING DATE: 2000-03-10
APPLICATION NUMBER: 09/839446
FILING DATE: 2001-03-19
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                                                                     ProLysGluGluHisCysTyrLeuLeu
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                                                                                                                                        IlePheThrPheGlyIleTrpGlnGlyAsnIleArgGluLeuAsnAspMetAlaSerThr
                                                                                                                                                                          GTGTTCATTGTCAGCACCGGCCGAGGCAACTTCCTGGAGCTGTCAGCCGCTGCCTCAGCC
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Application
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SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 194
LENGTH: 3568
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
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FILING DATE: 2001-03-29
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APPLICATION NUMBER: 09/863776
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FILING DATE: 2000-03-10
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PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195792
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PRIOR APPLICATION NUMBER: 099/863776
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 60/208263
PRIOR FILING DATE: 2000-05-31
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CURRENT FILING DATE: 2003-06-03
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                                                         GGTGAGGCTGCCCAG-----
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1: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*

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        US-10-453-372-2
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US-11-190-041-160
US-11-1131-826A-294
US-11-1131-82-449-9
US-11-192-449-9
US-11-192-449-9
US-11-192-449-9
US-11-192-240-34
US-11-102-240-34
US-11-02-240-34
US-11-02-240-34
US-11-02-240-34
US-10-453-372-186
US-10-453-372-186
US-10-453-372-178
US-10-453-372-196
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Sequence 2, Appli
Sequence 26, Appl
Sequence 294, App
Sequence 39, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 34, Appli
Sequence 34, Appli
Sequence 186, Appli
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11-193-857-19	-11-193-806-19	-11-193-789	11-193-771	-11-193-561	US-10-995-561-627	-10-995-561-62	-85	US-11-193-806-21	US-11-193-789-21	11-193-771-21	US-11-193-561	1-193-857-38	US-11-193-806-38	-193-789	US-11-193-771-38	-11-193-561	US-10-995-561-621	-56
7-19	5-19	9-19	1-19	1-19	1-62	1-62	7-21	5-21	9-21	1-21	1-21	7-38	5-38	9-38	1-38	1-38	1-62	1-628
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ALIGNMENTS

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; ORGANISM: Homo sapiens US-10-453-372-2
                                                                                        Query Match
Best Local Similarity
Matches 418; Conserv
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NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSeqList version
SEQ ID NO 2
LENGTH: 445
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Publication No. US20060003323A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO FILE REFERENCE: 21402-589 A CURRENT PAPLICATION NUMBER: US/10/453,372 CURRENT FILING DATE: 2003-06-03 PRIOR APPLICATION NUMBER: 09/789390 PRIOR FILING DATE: 2001-02-23 PRIOR PRIOR PRIOR DATE: 2001-03-29 PRIOR PRIOR DATE: 2000-03-01 PRIOR PRIOR DATE: 2000-03-01 PRIOR PRIOR DATE: 2000-03-01 PRIOR PRIOR DATE: 2000-03-01 PRIOR PRIOR DATE: 2001-03-29 PRIOR APPLICATION NUMBER: 06/195792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/839446
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/199476
PRIOR FILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 09/863776
PRIOR FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-08-25
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PRIOR FILING DATE: 2001-08-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-05-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/208263
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MLPWTALGLALSLRLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQL
                         MLPWTALGLALSLRLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQL
                                                                                             Conservative
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Pred. No. 3.9e-161;
0; Mismatches 0;
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61

VAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYA 120

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APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Mustrone J.
APPLICANT: Mustrone J.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PRIPITE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PRIPITE OF INVENTION HERRAPY OF COLON CANCER
FILLE REFERENCE: MPMO1-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT APPLICATION NUMBER: US/10/301,822
PRIOR APPLICATION NUMBER: US/0/301,822
PRIOR APPLICATION NUMBER: US/0/301,971
PRIOR APPLICATION NUMBER: US/0/301,971
PRIOR APPLICATION NUMBER: US/0/301,978
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR PRILING DATE: 2002-05-20
NUMBER: US/0/381,988
PRIOR PILING DATE: 2002-05-20
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 3063
TYPE: PRT
ORGANISM: Homo Sapiens
US-11-186-284-26
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US-11-186-284-26
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                                                                                                                                                Matches
                                                                                                                                                                 Query Match
Best Local
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SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVMVTDGGSSSDPV
                                                              KADIVFLVDGSYSIGIANFVKVRAFLEVLVKSFEISPNRVQISLVQYSRDPHTEFTLKKF
                                                                                         RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLFLGTGALRASLVHVGSRPYTEFPFGQH
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                                                                                                                                              Conservative
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US-11-169-041-160
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TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
TITLE OF INVENTION: CELLS
FILE REFERENCE: 10001 NP
CURRENT APPLICATION NUMBER: US/11/169,041
CURRENT FILING DATE: 2005-06-28
PRIOR APPLICATION NUMBER: 60/584,405
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 527
SOFTWARE: Patentin version 3.2
SEQ ID NO 160
LENGTH: 517
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                                                                                                                                                                                                                                                                                                                                                                                                           Matches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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      TVVEPASSTSVVLNSLKPETLYLVNVTAEYEDGFSIPLAGEETTEEVKGAPRNLKVTDET
                                           ----PGNATDWIWAGLDPDTDYDVALVPESNVRLLRPQILRVRTRPEEAGPERIVISHAR 317
                                                                                 QELAAIKKKAYVPPKDLSFSEVTSYGFKTNWSPAGENVFSYHI-----TYKEAAGDDEV
                                                                                                                       --LDAMR-----PQQLHATEITSSGFRLAWPPLLTADSGYYVLELVPSAQPGAARRQQL 261
                                                                                                                                                                 IKLRNSDVEIFAVGVKDAVDSELEAIASPPAETHVFTVEDFDAFQRISFELTQSICLRIE
                                                                                                                                                                                                      QELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGSI-----
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PRIOR APPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/049911
PRIOR PILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/076974
PRIOR PILING TO
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US-10-131-826A-294
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LENGTH: 915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                                                                         ORGANISM: Homo Sapien
                                                                                                                                                                           TYPE: PRT
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APPLICATION NUMBER: 60/059117
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                                16 ALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASL
                                                                                    Similarity
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ALLESSCEN-----KRADLVFIIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGL
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DeForge, Laura
Desnoyers, Luc
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                                                                                    11.8%;
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                                                               Score 253.5; Db o;
Pred. No. 2.1e-12;
"Mismatches 85;
                                                                                                      Length 915;
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RESULT 5
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LENGTH: 956
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CURRENT FILING DATE: 2005-04-21
PRIOR APPLICATION NUMBER: 60/256,704
PRIOR FILING DATE: 2000-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gangolli et al. TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
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PRIOR APPLICATION NUMBER: 60/257,314
PRIOR FILING DATE: 2000-12-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 190
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                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                Local
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APPLICATION NUMBER: 60/294,075
FILING DATE: 2001-05-29
APPLICATION NUMBER: 60/288,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/315,617
FILLING DATE: 2001-08-29
APPLICATION NUMBER: 60/307,506
FILING DATE: 2001-07-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/322,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 VANFSQIETLTSVFQK 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 -GVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL-- 190
  219 VANFSQIETLTSVFQK
                                      191 --HFVDVDDLHIIVQE
                                                                            159
                                                                                                              134 -GVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL--
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                                                                                                                                                     99 LQYGSTVKNEFSLKTFKRKSEVERAVKRMRHLSTGTMTGLAIQYALNIAFSEAEGARPLR 158
                                                                                                                                                                                           76 VHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARP--
                                                                                                                                                                                                                                 45 ALLESSCEN-----KRADLVFIIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGL
                                                                                                                                                                                                                                                     16 ALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASL
                                                                                                                                                                                                                                                                                                              62;
                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --HFVDVDDLHIIVQE 204
                                                                            ENVPRVIMIVIDGRPQDSVAEVAAKARDIGILIFAIGVGQVDFNTLKSIGSEPHEDHVFL
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No. US20050260713A1
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                            11.8%; Score 253.5; DB 7
31.6%; Pred. No. 2.2e-12;
tive 36; Mismatches 85
  234
                                                                                                                                                                                                                                                                                                                                                  DB 7;
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                                                                                                                                                                                                                                                                                                                                                  Length 956;
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; Sequence 6, Application US/11192449

RESULT 6 US-11-192-449-6

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APPLICANT: Gotwals, Philip
APPLICANT: Koteliansky, Victor
TITLE OF INVENTION: Method for the Treatment of Fibrosis
FILE REFERENCE: A073-USCN3
CURRENT APPLICATION NUMBER: US/11/192,449
CURRENT FILING DATE: 2005-07-28
PRIOR APPLICATION NUMBER: 10/625,260
PRIOR FILING DATE: 2003-07-22
PRIOR APPLICATION NUMBER: 10/061,658
PRIOR APPLICATION NUMBER: 09/557,092
PRIOR APPLICATION NUMBER: 09/557,092
PRIOR APPLICATION NUMBER: 09/557,092
PRIOR APPLICATION NUMBER: 60/130,847
PRIOR APPLICATION NUMBER: 60/137,214
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US-11-192-449-9
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Matches
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SEQ ID
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GENERAL INFORMATION:
  SOFTWARE:
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PRIOR TILING DATE: 2003-07-22
PRIOR APPLICATION NUMBER: 10/061,658
PRIOR FILING DATE: 2002-02-01
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                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Biogen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 10
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PRIOR FILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 60/130,847
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TYPE: PRT
ORGANISM: Homo sapien
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APPLICATION NUMBER: 60/137,214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
                      FastSEQ for Windows Version 4.0
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33.5%; Pred. No. 1.6e-08;
ative 28; Mismatches 77
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US-11-192-449-5
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Matches
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SEQ ID NO 5
LENGTH: 214
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APPLICANT: Biogen, Inc.
APPLICANT: Gotwals, Pr
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 10/625,260
PRIOR FILING DATE: 2003-07-22
PRIOR APPLICATION NUMBER: 10/61,658
PRIOR FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/557,092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Koteliansky, Victor
TITLE OF INVENTION: Method for the Treatment
FILE REFERENCE: A073-USCN3
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TYPE: PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/137,214 PRIOR FILING DATE: 1999-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 60/130,847
PRIOR FILING DATE: 1999-04-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/11/192,449
CURRENT FILING DATE: 2005-07-28
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ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                Local
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                                          140 LKQVIQDCEDENIQRFSIAILGHYNRGNLSTEKFVEEIKSIASEPTEK--HFFNVSDELA 197
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198 LHIIVQEL
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                                                                                                                                                                       94 GEAAQDAVRASAQRMG-DTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSD--P
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                                                                                                                                                                                                                    22 DIVIVIDGSNSI--YPWESVIAFLNDLLKRMDIGPKQTQVGIVQYGENVTHEFNLNKYSS
                                                                                                                                                                                                                                                               34 DIMFILDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS
                                                                                                                                                                                                                                                                                                            60;
                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                   VGPPMQELKDLGVTVFIVST----GRGNFL-----ELSAAASAPAEKHLHFVDVDD--- 197
                                                                                                                              TEEVLVAAKKIGRQGGLQTMTALGIDTARKEAFTEARGARRGVKKVMVIVTDGESHDNYR 139
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33.5%;
                                                                                                                                                                                                                                                                                                         8.6%; Score 185; DB 7; 31.9%; Pred. No. 8e-08; tive 32; Mismatches 76;
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Pred. No. 1.6e-08;
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US-11-102-240-34
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                                                                                                                                                                                                                                                                                                                                    Sequence 34, Application US/11102240 Publication No. US20050260647A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 34
LENGTH: 678
      APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS
TITLE OF INVENTION: ESOPHAGEAL TUMOR
TILE OF INVENTION: ESOPHAGEAL TUMOR
TILE OF INVENTION: UNMBER: US/11/102,240
CURRENT FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 10/063662
PRIOR APPLICATION NUMBER: 10/063667
PRIOR FILING DATE: 2001-12-06
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: PCT/US00/23328
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Best Local
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APPLICANT:
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CURRENT FILING DATE: 2002-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3230R1C1
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ORGANISM: Homo Sapien
FILING DATE: 2000-08-24
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ilarity 29.9%;
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; Pred. No. 4.4e-07;
26; Mismatches 99
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                                                                                    ; ORGANISM: Homo sapiens US-10-453-372-186
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PRIOR FILING DATE: 199-12-09
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 34
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NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 186
                  Query Match
Best Local Similarity
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195792
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CURRENT FILING DATE: 2003-06-03
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TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES,
                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/227800 PRIOR FILING DATE: 2000-08-25
                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-08-24
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PRIOR APPLICATION NUMBER: 09/939398
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PRIOR FILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 09/863776
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                                                                                                                          TYPE: PRT
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TYPE: PRT
                                                                                                                                                   LENGTH: 709
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o. US20060003323A1
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8.1%; Score 175; DB 6;
29.3%; Pred. No. 2.4e-06;
ative 34; Mismatches 94
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US-10-453-372-180
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LENGTH: 709
TYPE: PRT
ORGANISM: Homo s
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CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: 09/789390
PRIOR APPLICATION NUMBER: 09/789390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Alsobrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES,
FILE REFERENCE: 21402-589 A
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SOFTWARE: CuraSeqList version 0.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-08-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/839446 FILING DATE: 2001-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 09/823187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/227800
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    178
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                                                                                                                                 101 VPTATRVAIVTFSSKNYVVPRVDYISTRRARQHKCALLLQEIPÄISYRGGGTYTKGAFQQ 160
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                                                                                                                                                                         67 GTGALRASLVHVGSRPYTEFPFGQHSSGEAAQ-----DAVRASAQRMGDTHTGLALVY 119
                                                                                                                                                                                                                   49
                                                                                                                                                                                                                                                              7 LGLALSIRLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPL
                                                                                                                                                                                                                                                                                                        68;
                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YAKEQLFAEASGAREGVEKVLVWVTDGGSS---DEVGEEMQELKDLGVTVFIVSTGRGNFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPTATRVAIVTFSSKNYV-VPRADYISTRRARQHKCALLLQEIPAISYRGGGTYTKGAFQ 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGALRASLVHVGSRPYTEFPFGQHSSGEAAQ-----DAVRASAQRMGDTHTGLALV 118
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  LSAAASAPAEKHLHFVDVDDLHIIVQELRGSILDAMRPQQLHATEITSSGF 228
                                              AAQILL----HARENSTKVVFLITDGYSNGGDP-RPIAASLRDSGVEIFTFGIWQGNIRE
                                                                                    AKEQLFAEASGARPGVPKVLVWVTDGGSS--DPVGPPMQELKDLGVTVFIVSTGRGNFLE
                                                                                                                                                                                                                      LGQAFRRRVRLLRELSE-----RLELVFLVDDSSSVGEVNFRSELMFVRKLLSDFPV
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o. US20060003323A1
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                                                                                                                                                                                                                                                                                                      8.1%; Score 174; DB 6; 1
29.4%; Pred. No. 2.9e-06;
tive 33; Mismatches 96;
                                                                                                                                                                                                                                                                                                    Pred. No. 2.96
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----RLELVFLVDDSSSVGEVNFRSELMFVRKLLSDFPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          See File Wrapper or PALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEIC
                                                                                                                                                                                                                                                                                                                                              Length 709;
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US-11-080-026-4
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US-10-453-372-182
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Best Local Similarity
Thes 74; Conserve
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  PRIOR APPLICATION NUMBER: 09/789390
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR HILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 06/195792
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/839446
                                                                                                                                                                                                                                                                                                      Sequence 182, Application US/10453372 Publication No. US20060003323A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version SEQ ID NO 4
LENGTH: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Springer, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/11080026 Publication No. US20050260192A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: L1, Chafen

TITLE OF INVENTION: MODIFIED POLYPEPTIDES STABILIZED IN A

TITLE OF INVENTION: DESIRED CONFORMATION AND METHODS FOR

FILE REFERENCE: CFBF-P02-021

CURRENT APPLICATION NUMBER: US/11/080,026

CURRENT FILING DATE: 2005-03-15

PRIOR APPLICATION NUMBER: 09/945,265

PRIOR APPLICATION NUMBER: 09/945,265

PRIOR FILING DATE: 2001-08-31

PRIOR APPLICATION NUMBER: US 60/229,700

PRIOR APPLICATION NUMBER: US 60/229,700
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APPLICANT:
                                                                                                                                                                                                                 TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, FILE REFERENCE: 21402-589 A CURRENT APPLICATION NUMBER: US/10/453,372
                                                                                                                                                                                               CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                      APPLICANT: Alsobrook, et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 IHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 ALRGCPQEDSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLF--SLMQYSEEFR 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 TEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFABASGARPGVPKVLVWVT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 -- RG-----DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 VPVEAVNMSLGLSLAATTSPPQLLACGPTVHQTCSENTYVKGLCFLFGSNLRQQPQKFPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEALKTIONQLREKIF-AIEGTOTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSY
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                                                                                                                                                                                               2003-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.1%; Score 174; DB 7;
25.0%; Pred. No. 5.5e-06;
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AND METHOD

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RESULT 15
US-10-601-368-18
US-10-601-368-18
; Sequence 18, Application US/10601368
; Publication No. US20050260702A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-601-368-18
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NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 182
LENGTH: 709
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                     Query Match 8.0%; Score 172.5; DB 6; Length 1167; Best Local Similarity 24.0%; Pred. No. 7.3e-06; Matches 90; Conservative 47; Mismatches 119; Indels 119;
                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 1167
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                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/601,368
CURRENT FILING DATE: 2003-06-23
PRIOR APPLICATION NUMBER: US/09/561,263A
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/322,790
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 40
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TITLE OF INVENTION: NOVEL INTEGRIN ALPHA SUBUNIT AND USES THEREOF
FILE REFERENCE: 07334-275001
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FILING DATE: 2001-08-24
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FILING DATE: 2001-05-23
APPLICATION NUMBER: 60/208263
FILING DATE: 2000-05-31
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APPLICATION NUMBER: 60/199476
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                                           143 ARVDASFQPQGSLAPTAQRCPTYMDVVIVLDGSNSI--YPWSEVQTFLRRLVGKLFIDPE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 LSAAASAPAEKHLHFVDVDDLHIIVQELRGSILDAMRPQQLHATEITSSGF 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 AAQILL----HARENSTKVVSLITDGYSNGGDP-RPIAASLRDSGVEIFTFGIWQGNIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 AKEQLFAEASGARPGVPKVLVWVTDGGSS--DPVGPPMQELKDLGVTVFIVSTGRGNFLE 177
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ALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMG-DTHTGLALVYAKEQLFAEA 128
                                                                        ARSGAERGPPAS-APRG------DIMFILDSSASVSHYEFSRVREFVGQLVAPLPLGTG 69
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	333 AALGYHVQFGPLRGG 347	333	Ş
428	EGGHRLFPPRMALEDEFPPALQNHA 428	404	망
332	274 DPDTDYDVALVPESNVRLLRPQILRVRTRPEEAGPERIVISHARPRSLRVSWAPAL-GSA 332	274	Ş
403	SSFGLEMSQIGFSTHRLKDGILFGMVGAYDWGGSVLWL 403	366	Ъ
273	TSSGFRLAWPPLLTADSGYYVLELVPSAQPGAARRQQLPGNATDWIWAGL 273	224	Ş
365	RDPSSFLREIRTIASDPDERFFFNVTDEAALTDIVDALGDRIFGLEGSHAENE 365	313	В
223	ELSAAASAPAEKHLHFVDVDDLHIIVQELRG	177	Ş
312	261 HGGRPEAARLLVVVTDGESHDGEELPAALKACEAGRVTRYGIAVLGHYLRRQ 312	261	망
176	129 SGARPGVPKVLVWVTDGGSSDPVGPPMQBLKDLGVTVFIVSTGRGNFL 176	129	δ
260	201 QIQVGLVQYGESPVHEWSLGDFRTKEEVVRAAKNLSRREGRETKTAQAIMVACTEGFSQS 260	201	뫄

Search completed: February 13, 2006, 13:12:59 Job time : 10.087 secs

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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
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Published_Applications_AA_New:*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

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5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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913
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

45	44	43	42	41	40	39	38	37	36	35	3. <u>4</u>	33	32	<u>ω</u>	30	29	28	27	6
128	131	133	133	133	133.5	133.5	144.5	144.5	144.5	144.5	144.5	144.5	144.5	144.5	144.5	145.5	149.5	149.5	149.5
14.0	14.3	14.6	14.6			14.6	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.9	16.4	16.4	16.4
1167	184	1170	1170	184	1196	1179	2919	2813	2764	1188	1188	1188	1166	1141	182	1147	1188	1166	1141
7	σ	7	7	σ	9	7	σ	σ	σ	7	7	σ	σ	σ	σ	σ	σ	σ	σ
US-11-097-125-2	US-10-665-658-8	US-11-107-028-4	US-11-080-026-2	US-10-665-658-7	US-10-995-561-921	US-11-097-125-1	US-10-821-234-1133	US-10-995-561-688	US-10-995-561-691	US-11-000-463-810	US-11-000-463-338	US-10-601-368-3	US-10-601-368-4	US-10-601-368-6	US-10-601-368-7	US-10-453-372-4	US-10-601-368-21	US-10-601-368-22	US-10-601-368-24
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 Appli 	8, Appli	4, Appli	 Appli 	7, Appli	921, App	1, Appli	1133, Ap	688, App	691, App	810, App	338, App	3, Appli	4, Appli	6, Appli	7, Appli	4, Appli	21, Appl	22, Appl	rddw ' +2

ALIGNMENTS

RESULT 1 US-10-453-372-2

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PRIOR FILING DATE: 2001-02-23
PRIOR PRIOR APPLICATION NUMBER: 09/789390
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR PRIOR PRIOR DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/839446
PRIOR APPLICATION NUMBER: 09/839446
PRIOR APPLICATION NUMBER: 09/839476
PRIOR APPLICATION NUMBER: 09/83976
PRIOR APPLICATION NUMBER: 09/83776
PRIOR APPLICATION NUMBER: 09/863776
PRIOR APPLICATION NUMBER: 09/863776
PRIOR APPLICATION NUMBER: 09/98398
PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 09/93998
PRIOR APPLICATION NUMBER: 09/93998
PRIOR APPLICATION NUMBER: 60/227800
PRIOR APPLICATION NUMBER: 60/227800
PRIOR PILING DATE: 2000-08-25
PRIOR PILING DATE: 2000-08-25
PRIOR PILING DATE: 2000-08-25
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SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 2
                                                                                                                                                       Query Match
Best Local Similarity
Matches 180; Conserv
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APPLICANT: Alsobrook, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FILE REFERENCE: 21402-589 A CURRENT APPLICATION NUMBER: US/10/453,372 CURRENT FILING DATE: 2003-06-03
                                                                                                                                                                                                                                                                                                               TYPE: PRT
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  19
                                                     32
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                                               SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 120
                                                                                                                                                    100.0%; Score 913; DB 6; ilarity 100.0%; Pred. No. 1.4e-83; Conservative 0; Mismatches 0;
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US-11-169-041-160
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US-11-186-284-26
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PRIOR FILLING DATE: 2002-11-21
PRIOR PPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/381,988
                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                      Sequence 160, Appublication No.
TITLE OF INVENTION: KINASES AND, ...
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
FILE REFERENCE: 10001 NP
CURRENT APPLICATION NUMBER: US/11/169,041
CURRENT APPLICATION NUMBER: 2005-06-28
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Best Local Similarity
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                                                                                                                                                  APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: MPM01-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
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APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION,
TITLE OF INVENTION: THERAPY OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Millennium Pharmaceuticals, APPLICANT: Berger, Allison APPLICANT: Guillemette, Tracy L. APPLICANT: Kamatkar, Shubhangi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          438 KADIVFLVDGSYSIGIANFVKVRAFLEVLVKSFEISPNRVQISLVQYSRDPHTEFTLKKF
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Schlegel, Robert
Monahan, John E.
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                                                                                                                                                                                                                                                      US20060019284A1
                                                                                                KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.9%; Score 263.5; DB 7; 35.8%; Pred. No. 1.1e-17; tive 30; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 294, Application US/10131826A Publication No. US20050245730A1
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                                                                                                                                                                                                                                                               APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
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APPLICANT:
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PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 527
                                                                                      PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
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TYPE: PRT
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                                           APPLICATION NUMBER: 60/059263 FILING DATE: 1997-09-18
FILING DATE:
                     APPLICATION NUMBER: 60/059352
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Watanabe, Colin K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith, Victoria
Stewart, Timothy A.
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1997-09-19
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Pred. No. 4.1e-18;
"" amatches 83;
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Best Local S
Matches 58
                                                                                                                                                             Query Match
Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                         SEQ ID NO 39
LENGTH: 956
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 294
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PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/257,314
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2000-12-20
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PRIOR FILING DATE: 2000-12-19
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CURRENT FILING DATE: 2005-04-21
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                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 190
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FILING DATE: 2001-05-02
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FILING DATE: 2001-09-14
APPLICATION NUMBER: 60/294,075
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APPLICATION NUMBER: 60/315,617
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                                    SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARP---GVPKVLVWVTDGGSS 117
                                                                                                                    RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
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KRKSEVERAVKRMRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQ 174
                                                                             RADLVFIIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTF 114
                                                                                                                                                               Conservative
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                                                                                                                                                             27.5%; Score 251.5; DB 7
32.2%; Pred. No. 3.7e-17;
ative 36; Mismatches 79
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                                                                                                                                                                                                    DB 7;
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APPLICANT: Biogen, Inc.
APPLICANT: Gotwals, Philip
APPLICANT: Gotwals, Philip
APPLICANT: Gotwals, Prictor
TITLE OF INVENTION: Method for the Treatment of
FILE REFERENCE: A073-USCN3
CURRENT APPLICATION UNMBER: US/11/192,449
CURRENT FILING DATE: 2005-07-28
PRIOR APPLICATION NUMBER: 10/625,260
PRIOR APPLICATION NUMBER: 10/661,658
PRIOR APPLICATION NUMBER: 10/061,658
PRIOR APPLICATION NUMBER: 10/061,658
PRIOR FILING DATE: 2002-02-01
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US-11-192-449-9
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PRIOR FILING DATE: 2003-07-22
PRIOR APPLICATION NUMBER: 10/061,658
PRIOR FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/557,092
PRIOR FILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 60/130,847
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/137,214
PRIOR APPLICATION NUMBER: 60/137,214
PRIOR FILING DATE: 1999-06-01
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                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/11192449
Publication No. US20050281818A1
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Best Local Similarity
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 TEEVLVAAKKIVQRGGRQTMTALGTDTARKEAFTEARGARRGVKKVMVIVTDGESHDNHR 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 DIVIVLDGSNSI--YPWDSVTAFLNDLLKRMDIGPKQTQVGIVQYGENVTHEFNLNKYSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LHIIVQEL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEAAQDAVRASAQRMG-DTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSD--P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.2%; Score 194; DB 7;
33.5%; Pred. No. 2.7e-12;
tive 28; Mismatches 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
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                                                                                                                                                              ; TYPE: PRT ; ORGANISM: Rat US-11-192-449-5
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US-11-192-449-5
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TYPE: PRT
ORGANISM: Homo sapien
US-11-192-449-9
                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/11/192,449
CURRENT FILING DATE: 2005-07-28
PRIOR APPLICATION NUMBER: 10/625,260
PRIOR FILING DATE: 2003-07-22
PRIOR APPLICATION NUMBER: 10/061,658
PRIOR APPLICATION NUMBER: 00/557,092
PRIOR PILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/557,092
PRIOR APPLICATION NUMBER: 60/130,847
PRIOR APPLICATION NUMBER: 60/130,847
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
                                                                                   Matches
                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                    SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Biogen,
APPLICANT: Gotwal:
APPLICANT: Koteli
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PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 10
SOPTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Koteliansky, Victor TITLE OF INVENTION: Method for the Treatment FILE REFERENCE: A073-USCN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/557,092
PRIOR FILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 60/130,847
PRIOR FILING DATE: 1999-04-22
                                                                                                                                                                                                                          LENGTH: 214
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                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/137,214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 LKKVIQDCEDENIQRFSIAILGSYNRGNLSTEKFVEEIKSIASEPTEK--HFFNVSDELA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 VGPPMQELKDLGVTVFIV----STGRGNFL-----ELSAAASAPAEKHLHFVDVDD--- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 TEEVLVAAKKIVORGGROTMTALGTDTARKEAFTEARGARRGVKKVMVIVTDGESHDNHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
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                                                                                                    Similarity
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                                      DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEAAQDAVRASAQRMG-DTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSD--P 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVTIVKTL
DIVIVLDGSNSI--YPWESVIAFLNDLLKRMDIGPKQTQVGIVQYGENVTHEFNLNKYSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gotwals, Philip
                                                                                 Conservative
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                                                                                                                                                                                                                                                                     for Windows
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                                                                                                  20.3%;
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33.5%; Pred. No. 2.7e-12;
tive 28; Mismatches 77
                                                                             Score 185; DB 7; Length 214; Pred. No. 2.1e-11; 32; Mismatches 76; Indels
                                                                                                                                                                                                                                                                     Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Fibrosis
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RESULT 10
US-11-102-240-34
; Sequence 34, Application US/11102240
; Publication US20050260647A1
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US-10-063-703-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/063,703
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 34
SEQ ID NO 34
                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                     FILE REFERENCE: P3230R1C106C
CURRENT APPLICATION NUMBER: US/11/102,240
CURRENT FILING DATE: 2005-04-08
                                                                                                                                 APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Eaton, Dan L. APPLICANT: Filvaroff, E
                                                                                       TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS TITLE OF INVENTION: ESOPHAGEAL TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 LKQVIQDCEDENIQRFSIAILGHYNRGNLSTEKFVEEIKSIASEPTEK--HFFNVSDELA 197
                                                                                                                                                                                                                                                                                                                                                                                                           612 PAMAAHLKGVITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRI 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    555 KPDILNAIKRVGYWSGGTSTGAAINFALEOLFKK---SKPNKRKLMILITDGRSYDDVRI 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             495 DIGFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTDTRIGAVQYTYEQRLEFGFDKYSS 554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVD-VDDLHIIVQEL 174
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Grimaldi, Christopher J.
Gurney, Austin L.
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Gerritsen, Mary E.
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Pred. No. 1.6e-10;
5; Mismatches 91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 678
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US-10-453-372-186
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 Query Match
Best Local S
Matches 54
                                                                                                                  SOFTWARE: CuraSeqList
SEQ ID NO 186
LENGTH: 709
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Best Local Similarity
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SEQ ID NO 34
                                                                     TYPE: PRT
ORGANISM: Homo
-10-453-372-186
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                                                                                                                                                                       Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Alsobrook,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/789390
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                                                                                                                                                                                                           FILING DATE: 2000-08-25
                                                                                                                                                                                                                                                                                                                          FILING DATE: 2000-03-25
APPLICATION NUMBER: 09/863776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/185967
                                                                                                                                                                                                                         APPLICATION NUMBER: 60/227800
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/208263
FILING DATE: 2000-05-31
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/199476
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 09/839446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/823187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2002-05-07
APPLICATION NUMBER: 10/006867
FILING DATE: 2001-12-06
APPLICATION NUMBER: PCT/US00/23328
FILING DATE: 2000-08-24
APPLICATION NUMBER: 60/170262
                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/939398
                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/195792
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2001-03-29
                                                                                                                                                                                                                                             FILING DATE:
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   l Similarity
54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS
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     Conservative
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17.9%; Score 163; DB 6; 31.4%; Pred. No. 1.7e-08; tive 27; Mismatches 75;
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                                 Length 709;
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; LENGTH: 1152
; TYPE: PRT
GENERAL INFORMATION:
APPLICANT: Alsobrook, et al.
APPLICANT: Alsobrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES,
FILE REFERENCE: 21402-589 A
CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: 09/789390
                                                                                                                                                                                          Sequence 180, Appropriation No.
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PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,700
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/11/080,026
CURRENT FILING DATE: 2005-03-15
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APPLICANT: Lu, Chafen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 NPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLG
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28.1%; Pred. No. 3.6e-08;
rative 31; Mismatches 91; Indels 11;
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; ORGANISM: Homo sapiens
US-10-453-372-180
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LENGTH: 709
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SOFTWARE: CuraSeqList version 0.1
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                                           APPLICATION NUMBER: 60/208263
FILING DATE: 2000-05-31
APPLICATION NUMBER: 09/939398
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/185967 FILING DATE: 2000-03-01
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APPLICATION NUMBER: 60/199476
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FILING DATE: 2000-05-31
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o. US20060003323A1
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                                                                                                                                          ; ORGANISM: Homo US-10-453-372-178
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NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 194
LENGTH: 3568
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LENGTH: 3570
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PRIOR
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                                                                                                                                                                                                                                                   Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 1609
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/227800 PRIOR FILING DATE: 2000-08-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Alsobrook, et al.
                                                                                                                                                                                                                                  SOFTWARE:
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                                                                                        Similarity
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RLELVFLVDDSSSVGEVNFRSELMFVRKLLSDFPVVPTATRVAIVTFSSKNYVVPRVDYI 137
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Search Job tim	Db	Ş	₽	Ş
Search completed: February 13, 2006, 13:12:58 Job time : 3.91304 secs	194 GYSNGGDP-RPIAASLRDSGVEIFTFGIWQGNIRELNDWASTPKEEHCYLL 243	114 GGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV 162	138 STRRAROHKCALLLQEIPAISYRGGGTYTKGAFQQAAQILLHARENSTKVVFLITD 193	61 SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVMVTD 113
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-Og-/abss/ABSSWEB spool/US10699035/runat_13022006_062453_25634/app_query.fasta_1
-Og-/abss/ABSSWEB spool/US10699035/runat_13022006_062453_25634/app_query.fasta_1
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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US-11-186-284-26

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US-11-182-016-20

US-10-131-826A-294

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US-10-821-234-1431

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Sequence 26, Appl
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Sequence 20, Appl
Sequence 294, App
Sequence 39, Appl
Sequence 1431, App
Sequence 31, Appl
Sequence 35, Appl
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ALIGNMENTS

US-10-453-372-2

Sequence 2, Application US/10453372

Publication No. US20060003323A1

GENERAL INFORMATION:

APPLICANT: Alsobrook, et al.

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHO

FILE REFERENCE: 21402-589 A

CURRENT FILING DATE: 2001-06-03

PRIOR FILING DATE: 2001-00-2-23

PRIOR PILING DATE: 2001-03-29

PRIOR PILING DATE: 2001-03-29

PRIOR PILING DATE: 2001-03-29

PRIOR PILING DATE: 2001-03-29

PRIOR PILING DATE: 2000-03-01

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PRIOR PILING DATE: 2001-03-25

PRIOR PILING DATE: 2001-03-25

PRIOR PILING DATE: 2001-03-25

PRIOR APPLICATION NUMBER: 09/8376

PRIOR PILING DATE: 2001-03-25

PRIOR PILING DATE: 2001-08-25

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Best Local Similarity:
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; ORGANISM: Homo
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                                                                                       GlyTyrTyrValLeuGluLeuValProSerAlaGlnProGlyAlaAlaArgArgGlnGln
                                                                                                                   GGCTACTATGTGCTGGAGCTGGTGCCCAGCGCCCAGCCGGGGCTGCAAGACGCCAGCAG
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   GTGGCCTAGTGCCTGAGTCCAACGTGCGCCTCCTGAGGCCCCAGATCCTGCGGGTGCGC
                            LeuProGiyAsnAlaThrAspTrpIleTrpAlaGlyLeuAspProAspThrAspTyrAsp
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APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: MCTHOL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: MCTHOL GENES, COMPOSITION, ASSESSM
TITLE OF INVENTION: THERAPY OF COLON CANCER
TITLE OF INVENTION UMBER: US/11/186,284
CURRENT APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-05-05
PRIOR FILING DATE: 2002-05-05
PRIOR FILING DATE: 2002-05-05
PRIOR FILING DATE: 2002-05-05
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                           ; ORGANISM: Homo US-11-186-284-26
    Score:
                  Pred. No.:
                              Alignment Scores:
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                                                                                                     SEQ ID NO 26
LENGTH: 3063
                                                                                       LENGTH: 30
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    Length:
Matches:
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ASSESSMENT,

PREVENTION,

AND

Db 698 LeuValAsnValThrAlaGluTyrGluAspGlyPheSerIleProLeuAlaGlyGluGlu 717 Qy 757	Percent Similarity: 39.98 Best Local Similarity: 27.58 Description: 174 Obery Match: 171.68 Description: 1
Oy 106 ATGTTCCTGCACAGCTCAGCCAGCGTCTCACCAGTTCCCCGGGTTCGGGAG 165	Db 758 ArgProValAlaGlyGlyGluSerArgSluValThrThrProProNanGlnArgArgArg 777 Qy 811

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RESULT 4
US-11-182-016-20
Sequence 20, Application US/11182016
Publication No. US20060019294A1
GENERAL INFORMATION:
APPLICANT: SUGEN, INC.
TITLE OF INVENTION: TYROSINE KINASE
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NUMBER OF SEQ ID NOS: 55
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR PFLICATION NUMBER: 60/056974
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SEQ ID NO 294
LENGTH: 915
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PRIOR APPLICATION NUMBER: 60/059115
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                                   59 ValPheIleIleAspSerSerArgSerValAsnThrHisAspTyrAlaLysValLysGlu
                                                                                                              45 AlaLeuLeuGluSerSerCysGluAsn-----
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Godowski, Paul
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Gurney,Austin L.
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Filvaroff, Ellen
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Publication No. US20050260713A1
GENERAL INFORMATION:
                                                                                                                                                                                     SEQ ID NO 39
LENGTH: 956
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TITLE OF INVENTION: Polypeptides and Nucleic Acids
FILE REFERENCE: 21402-225
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CURRENT FILING DATE: 2005-04-21
PRIOR APPLICATION NUMBER: 60/256,704
PRIOR FILING DATE: 2000-12-19
                                                                                                                                                                                                                            SOFTWARE: PatentIn
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ORGANISM: Homo
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R FILLING DATE: 2001-08-10
DR APPLICATION NUMBER: 60/257,314
DR FILLING DATE: 2000-12-20
DR APPLICATION NUMBER: 60/311,613
DR FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/288,153 FILING DATE: 2001-05-02
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APPLICATION NUMBER: 60/322,358
FILING DATE: 2001-09-14
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FILING DATE: 2001-08-29
APPLICATION NUMBER: 60/307,506
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                 Percent Similarity:
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 Query Match:
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                                                                                                                                                                                       SOFTWARE: pt_SEQ_genes Version
SEQ ID NO 1431
LENGTH: 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1431, Application US/10821234 Publication No. US20050255114A1 GENERAL INFORMATION:
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APPLICANT: Stache-Cra
APPLICANT: Andarmani,
ADDITCANT: Tanc V T
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PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ_ID NOS: 1704
                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tang, Y. Tom TITLE OF INVENTION: Methods for Diagnosis
                                                                                                                                                     ORGANISM:
                                                                                                                                                                       TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Publication No
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: MOVEL GENES, COMPOSITIONS, K.
TITLE OF INVENTION: METHODS FOR IDENTIFICATION,
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPMOL-029PZRNM
FILE REFERENCE: MPMOL-029PZRNM
                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 200 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: NOVEL GENES, COMPOSITION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPMO1-029P2RNM
CURRENT APPLICATION UNMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/0/339,971
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2002-13-05
PRIOR FILING DATE: 2002-05-20
PRIOR FILING DATE: 2002-05-20
INDRED OF SCOT TO NOC. 328
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Best Local Similarity:
Query Match:
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US-11-186-284-35
Sequence 35, Application US/11186284
Publication No. US20050266493A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
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Kamatkar, Shubhangi
Schlegel, Robert
Monahan, John E.
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APPLICANT: Wehrman, Tom
APPLICANT: Zhang, Jie
APPLICANT: Zhou, Jie
APPLICANT: Zhou, Jie
APPLICANT: Cao, Yi-Cheng
APPLICANT: Cao, Yi-Cheng
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 785C1F4CN
CURRENT FILING DATE: 2004-11-29
PRIOR APPLICATION NUMBER: US/11/000,463
CURRENT FILING DATE: 2002-11-08
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR APPLICATION NUMBER: 09/922,279
PRIOR APPLICATION NUMBER: 09/922,279
PRIOR APPLICATION NUMBER: 09/922,279
PRIOR APPLICATION NUMBER: 09/921,404
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/491,404
                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
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; ORGANISM: Homo
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US-11-000-463-243
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PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR APPLICATION NUMBER: 09/633,870
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1108 HisLeuGlyArgAlaGlyLysArgGlyLeu-----
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Asundi, Vinod
Chen, Rui-hong
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Wang, Zhiwei
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                                                                                                                                            GlyAlaThrGlyPheProGlyAlaAlaGlyArgValGlyProProGlyProSerGlyAsn
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CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILLING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR APPLICATION NUMBER: US 60/361,988
PRIOR FILING DATE: 2002-05-20
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Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals,
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows
SEQ ID NO 28
LENGTH: 1464
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APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASS
TITLE OF INVENTION: THERAPY OF COLON CANCER
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TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES
FILE REFERENCE: 06275-254US1
CURRENT APPLICATION NUMBER: US/11/021,603
CURRENT FILING DATE: 2004-12-21
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                                                                                              ProGlyThrProGlyProGlnGlyIleAlaGlyGlnArgGlyValValGlyLeuProGly
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                                                                                                                                                                                                                                                                                                                                               CGTGCAGTTCGGGCCGCTGCGGGGCGGGGAGGCGCAGCGGGT------
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APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Cao, Yi-Cheng
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Pol
FILE REFERENCE: 785CIP4CN
CURRENT APPLICATION NUMBER: US/11/000,463
CURRENT FILLING DATE: 2004-11-29
PRIOR APPLICATION NUMBER: 10/291,265
PRIOR FILLING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR APPLICATION NUMBER: 09/922,279
PRIOR APPLICATION NUMBER: 09/922,279
PRIOR APPLICATION NUMBER: 09/92,279
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                US-10-699-035A-5 (1-1254) x US-11-000-463-243 (1-1464)
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SOFTWARE: FastSEQ for
SEQ ID NO 243
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APPLICANT: Liu, Chenghua
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282 ProAlaGlyProLysGlyGluProGlySerProGlyGluAsnGlyAlaProGlyGlnMet
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Qian, Xiaohong E
Wang, Zhiwei
Wehrman, Tom
Zhang, Jie
Zhou, Ping
Cao, Yi-Cheng
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US-11-186-284-28
                                                                                                                                         Best Local Similarity:
Query Match:
                                                                               US-10-699-035A-5 (1-1254) x US-11-186-284-28 (1-1464)
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                                                                                                                                                                                    Percent Similarity:
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Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals,
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASS
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPMO1-029PZRMM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
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TYPE: PRT
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Search completed: February 13, 2006, 13:54:37 Job time: 43.2027 secs

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GenCore version (c) 1993 - 2006

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Result
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-Q=/Abss/ABSSWEB spool/US10699035/runat 13022006 062444 25463/app_query.fasta_1
-Q=/Abss/ABSSWEB spool/US10699035/runat 13022006 062444 25463/app_query.fasta_1
-DB=PIR -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -ALIGN=15 -MODE=LOCAL
-OCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINIEN=0 -MAXLEN=200000000 -HOST=abss02p
-USER=US10699035 @CGN 1 17 @runat 13022006 062444 25463 -NCPU=6 -ICPU=3
-NORMAP -NEG SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-MARN TIMEOUT=30 -THEADS=1 -XGAPOP=10 -XGAPDXT=0.5 -FGAPOP=6 -FGAPEXT=7
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A;Gene: CO:14A1

A;Gene: CO:14A1

A;Gene: CO:14A1

C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trim: C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trim: F;1-28/Domain: signal sequence #status predicted <SIG>
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F;29-110/Domain: fibronectin type III repeat homology <FN3B>
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F;534-614/Domain: fibronectin type III repeat homology <FN3B>
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F;741-823/Domain: fibronectin type III repeat homology <FN3B-A;Molecule type: mRNA
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A;Residues: 1-1857 <MAE>
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A;Cross-references: uniparc:upi000017123C; EMBL:X70792; NID:g288874; PIDN:CAA50063.1;
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C;Genetics: collagen alpha 1(XIV) chain precursor, short form - chicken c;Species: Gallus gallus (chicken) C;Species: Gallus gallus (chicken) C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003 C;Accession: S31212 R;Waselchli, C:; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B. Eur. J. Biochem. 212, 483-490, 1993 A;Title: Complete primary structure of chicken collagen XIV. A;Reference number: S31211; MUID:93185668; PMID:8444186 Percent Similarity: Best Local Similari A; Reference number: A; Accession: S31212 F;922-1009/Domain: fibronectin A;Status: nucleic acid sequence not Query Match: F;1040-1205/Domain: Genetics: No.: Similarity: von 1.15e-13 268.00 50.5% 33.0% 25.5% Willebrand factor shown; translation not shown III repeat homology <FN3H> actor type A repeat homology Length:
Matches:
Conservative:
Mismatches: < VWA2 >

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integrin alpha-1

< VWA2 >

197

217

237

177

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A;Residues: 1-416;1
A;Cross-references:
C;Genetics:
A;Gene: Coll4A1

C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycopr

F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1888/Product: collagen alpha 1(XIV) chain, long form #status predicted

F;29-110/Domain: fibronectin type III repeat homology <FN3A>

F;156-320/Domain: von Willebrand factor type A repeat homology <VWA1>
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A;Residues: 1-1888 <TRU>
A;Cross-references: UNIPROT:P32018; UNIPARC:UPI0000126D31; EMBL:X70793; NID:g288872;
A;Waelchli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: S31211; MUID:93185668; PMID:8444186
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$78476
$collagen alpha 1(XIV) chain precursor,
collagen alpha 1gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence revision
C;Accession: $78476; $31211
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A;Status: preliminary
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F;534-614/Domain: fibronectin type III r
F;623-707/Domain: fibronectin type III r
F;623-707/Domain: fibronectin type III re
F;741-823/Domain: fibronectin type III re
F;832-914/Domain: fibronectin type III re
F;922-1009/Domain: fibronectin type III re
F;1040-1205/Domain: von Willehrer-
  N;Alternate names: fibrochimerin
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C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A40020; A34485; B34485; A28037; S23814; S22\overline{5}54; S28811
R;Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nish:
J. Cell Biol. 115, 209-221, 1991
A;Title: The complete primary structure of type XII collagen shows a chimer:
nous region of type IX collagen, and short collagenous domains with an Arg-
A;Reference number: A40020; MUID:92011862; PMID:1918137
A;Accession: A40020
A;Molecule type: mRNA
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AlaAspPheAsnPheMetAsnSerIleValGluGlyLeuThrArgThrValCysSerArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt GlyLeuAlaGlnTyrSerGlyAspProArgIleGluTrpHisLeuAsnAlaTyrGlyThr}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ceeeaerriereeeccaecreereerccacrecccreeecacceeecccreeeisce 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                              ---GACGTGGATGACCTGCACATCATTGTCCAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspIleAsnGluLeuLysGluIleAlaSerGluProAspSerThrHisValTyrAsnVal
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                                               type XII collagen shows a chimeric molecule collagenous domains with an Arg-Gly-Asp site PMID:1918137
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t homology <FN3C>
t homology <FN3D>
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t homology <FN3E>
t homology <FN3F>
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F;437-601/Domain: ton Willebrand factor type A repeat homology <VW.
F;629-1178/Domain: IIIC #status predicted <IIIC>
F;630-711/Domain: fibronectin type III repeat homology <FN3C>
F;630-711/Domain: fibronectin type III repeat homology <FN3D>
F;721-802/Domain: fibronectin type III repeat homology <FN3D>
F;812-895/Domain: fibronectin type III repeat homology <FN3B>
F;905-986/Domain: fibronectin type III repeat homology <FN3B>
F;995-1076/Domain: fibronectin type III repeat homology <FN3B>
F;1086-1169/Domain: fibronectin type III repeat homology <FN3H>
F;1197-1361/Domain: von Willebrand factor type A repeat homology <FN3IS-
F;1384-1265/Domain: fibronectin type III repeat homology <FN3IS-
F;1384-1465/Domain: fibronectin type III repeat homology <FN3IS-
F;1474-1557/Domain: fibronectin type III repeat homology <FN3IS-
F;1566-1647/Domain: fibronectin type III repeat homology <FN3IS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:(PDI0000173246; EMBL:X67327
C;Genetics:
A;Introns: 2845/3; 2863/3; 2887/3; 2899/3; 2922/1; 2985/1; 3008/
C;Keywords: alternative splicing; cell binding; coiled coil; con:
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-3124/Product: collagen alpha 1(XII) chain #status predicted
F;24,1189-3124/Product: collagen alpha 1(XII) chain short splice
F;24-114/Domain: IIIA #status predicted <IIIA>
F;24-105/Domain: fibronectin type III repeat homology <FN3A>
F;332-414/Domain: von Willebrand factor type A repeat homology <FN3B>
F;332-414/Domain: fibronectin type III repeat homology <FN3B>
F;332-414/Domain: von Willebrand factor type A repeat homology <
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Biol. Chem. 262, 17724-17727, 1987
A;Title: Type XII collagen is expressed in A;Reference number: $22254; MUID:88087065; A;Accession: $22254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: The two splice variants of collagen XII share a A;Reference number: S28811; MUID:93042014; PMID:1420368 A;Accession: S28811
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A;Cross-references: UNIPROT:P13944; UNIPARC:UPI0000126D2D; GB:D00824; NID:g222810; PA;Cross-references: UNIPROT:P13944; UNIPARC:UPI0000126D2D; GB:D00824; NID:g222810; PA;Note: in the authors' translation residues 1216-1219 are shown after residue 1235 R;Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.

J. Biol. Chem. 264, 19772-19778, 1989

A;Reference number: A34485; MUID:90062079; PMID:2584192

A;Reference number: A34485; MUID:90062079; PMID:2584192

A;Accession: A34485

A;Molecule type: mRNA
A;Residues: 2456-2758,'A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
A;Accession: B34485
A;Molecule type: protein
A;Accession: B34485
A;Molecule type: protein
A;Accession: B34485
A;Molecule type: protein
A;Residues: 2772-2792;2846-2873 <GOR2>
A;Residues: 2772-2792;2846-2873 <GOR2>
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A;Title: A major oligomeric fibroblast proteoglycan identified as a novel large form of A;Reference number: $23814; MUID:92362621; PMID:1323460

A;Accession: $23814

A;Molecule type: protein

A;Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517

A;Cross-references: UNIPARC:UPI0000173C41; UNIPARC:UPI0000173C42; UNIPARC:UPI0000173C43
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A;Residues: 2960-2976,'F',2978-3074,'AG' <GOR3>
A;Residues: 2960-2976,'F',2978-3074,'AG' <GOR3>
A;Cross-references: UNIPARC:UPI00001712F4; EMBL:M17375; NID:g211649;
A;Note: this sequence has been revised in reference A34485
R;Koch; M.; Bernasconi, C.; Chiquet, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.24-114/Domain: IIIA #status predicted <IIIA>
7.24-105/Domain: fibronectin type III repeat homology <FN3A>
7.317-301/Domain: von Willebrand factor type A repeat homology <V
7.332-425/Domain: IIIB #status predicted <IIIP-
7.332-414/Domain: while brand factor type A repeat homology <V
7.332-414/Domain: while brand factor type A repeat homology <V
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;Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280
;Cross-references: UNIPARC:UPI0000173C46; EMBL:X67327
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;Residues: 2456-2758,'A',2760-2802,'F',2804-2976,'F',2978-3124 <GOR>
;Cross-references: UNIPARC:UPI0000171233; EMBL:J05137; NID:g211284; PIDN:AAA48635.1;
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F;2438-2440/Region:
F;2509-2750/Domain:
F;2751-2902/Domain:
F;2899-2901/Region:
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Query Match:
DB:
N;Alternate names: undulin
C;Species: Gallus gallus (chicken)
C;Species: To-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A45974; S30085; S22916; S17035; S20833
R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Canc. J. Biol. Chem. 268, 12177-12184, 1993
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F;1847-1928/Domain:
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non-collagemous NC1 #status predicted <NC1>
,1512,1767,2210,2273,2532,2683/Binding site:
h) 2860 2866.2869.3004,3007/Modified site: h)
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F;40-204/Domain: von Willebrand factor type A repeat homology <VW
F;236-4091/Domain: fibronectin type III repeat homology <FN3A>
F;326-4091/Domain: fibronectin type III repeat homology <FN3A>
F;418-498/Domain: fibronectin type III repeat homology <FN3C>
F;507-591/Domain: fibronectin type III repeat homology <FN3C>
F;625-707/Domain: fibronectin type III repeat homology <FN3E>
F;625-707/Domain: fibronectin type III repeat homology <FN3E>
F;806-893/Domain: fibronectin type III repeat homology <FN3F>
F;806-893/Domain: fibronectin type III repeat homology <FN3G-
F;924-1089/Domain: von Willebrand factor type A repeat homology <FN3G-
F;1111-1352/Domain: non-collagenous NC2 #status predicted <NC4>
F;1511-553/Domain: triple helical domain COL1 #status predicted
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C;Keywords: alternative splicing; coiled of F;40-204/Domain: von Willebrand factor type
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Eur. J. Biochem. 201, 333-338, 1991
A;Title: Cloning of a cDNA for a new member
A;Reference number: S17035; MUID:92037585; F
A;Accession: S17035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUR. J. Biochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of
A;Reference number: S22916; MUID:92339443;
A;Accession: S22916
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R;Apte, S.S.
submitted to the EMBL Data Library, March 1992
a-Reference number: S30085
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A;Residues: 1-1747 <GER>
A;Cross-references: UNIPROT:P32018; UNIPARC:UPI0000173C47
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Pred. No.:
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A; Residues: 1551-1570; 1593-1599; 1639-1667 < GOR2>
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A;Residues: 286-494,'Q',496-834,'A',836-1119,'KL',1122-1402,1409-1439
A;Cross-references: UNIPARC:UP10000173C48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1472-1660 <APT>
A;Residues: 1472-1660 <APT>
A;Cross-references: UNIPARC:UPI00000006A2; EMBL:X65122; NID:g62871; PIDN:CAA46238.1; PID
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                                                                                                                                                                                                                  US-10-699-035A-1 (1-537) x A45974
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A;Residues: 1472-1659 <GORl>
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                                                                                                                                                                         GACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTT
                                          ArgLeuPheLeuGluAsnLeuValSerArgPheAsnValGlySerGluLysThrArgVal
                                                                                    CGGGAGTTTGTGGGGCAGCTGGTGGCTCCACTGCCCCTGGGCACCGGGGCCCCTGCGTGCC
                                                                                                                               AspIleValIleLeuValAspGlySerTrpSerIleGlyArgPheAsnPheArgLeuVal
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PMID:1339349
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 78-493 <ARG>
A; Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A
F; 37-204/Domain: von Willebrand factor type A repeat homology <VWA1>
F; 270-434/Domain: von Willebrand factor type A repeat homology <VWA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kiss, I.; Deak, F.; Holloway Jr., R.G.; Delius, H.; Mebust, K.A.; Frimberger, E.; Argr J. Biol. Chem. 264, 8126-8134, 1989
A;Title: Structure of the gene for cartilage matrix protein, a modular protein of the exgrins, Von Willebrand factor, complement factors B and C2, and epidermal growth factor. A;Reference number: A33809; MUID:89255246; PMID:2542265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cartilage matrix protein precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C;Accession: A33809; A2364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Argraves, W.S.; Deak, F.; Sparks, K.J.; Kiss, I.; Goeti Proc. Natl. Acad. Sci. U.S.A. 84, 464-468, 1987. A;Title: Structural features of cartilage matrix protein A;Reference number: A26364; MUID:87092429; PMID:3025875 A;Accession: A26364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P05099; UNIPARC:UPI000004F1EF; GB:X12346; GB:X12347; GB:X123
R;Argraves, W.S.; Deak, F.; Sparks, K.J.; Kiss, I.; Goetinck, P.F.
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                                                                                                             US-10-699-035A-1 (1-537) x A33809
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AlaAspPheAsnPheMetAsnSerIleValGluGlyLeuThrArgThrValCysSerArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein A;Reference number: $66522; MUID:96270751; PMID:8665920 .
A;Accession: $66522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cartilage matrix protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S66522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Genetics:
A;Gene: CMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-500 < ASZ >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Biochem. 236, 970-977,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Aszodi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P51942; UNIPARC:UPI0000029480; EMBL:U35035; NID:g1163178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                     No.:
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                                                           CGGGAGTTTGTGGGGCAGCTGGTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGTGCC 123
                                                                                                                                               GACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrAlaAsp
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34.8%
22.8%
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Matches:
Conservative:
Mismatches:
Indels:
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C;Superfamily: cartilage matrix protein; EGF homology; von Willebrand C;Keywords: glycoprotein; homotrimer F;1-22/Domain: signal sequence #status predicted <SIG>F;23-496/Product: cartilage matrix protein #status predicted <MAT>F;39-206/Domain: von Willebrand factor type A repeat homology <VWA1>F;27-252/Domain: EGF homology <EGF>F;27-452/Domain: von Willebrand factor type A repeat homology <VWA2>F;76,344/Binding site: carbohydrate (Asn) (covalent) #status predicted F;221-238,234-247,249-262/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 157-290, 'L',292-496 <JE2>
A;Cross-references: UNIPARC:UPI000016A6E8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; J. Biol. Chem. 265, 19624-19631, 1990
A;Title: Structure and chromosomal location of the human A;Reference number: A37979; MUID:91060568; PMID:2246248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cartilage matrix protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Jul-1991 #sequence revision 12-Jul-1991 #text_change 09-Jul-2004
C;Accession: A37979; B37979
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; C; Complex: homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Map position: 1p35-1p35
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A; Residues: 1-496 <JEN>
A; Cross-references: UNIPROT: P21941; UNIPARC: UPI000004F1ED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A37979
                                                                      Query Match:
                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                         Score:
                                                                                                                                                                                     Alignment
  US-10-699-035A-1 (1-537)
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                                                7.02e-11
233.50
50.3%
35.0%
22.3%
x A37979
  (1-496)
                                                                                                               Length:
Matches:
Conservative:
                                                Gaps:
                                                                                         Mismatches:
                                                                        Indels:
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62
27
87
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C;Species: Homo sapiens (man)
C;Date: 04-Nov-1994 #sequence revision 04-Nov-1994 #text change
C;Accession: A54849; PH0844; S16316; I56328; A30296; I84886
C;Accession: A.M.; Greenspan, D.S.; Lee, S.; Uitto, J.
                                                                                                                                                                A;Note: the authors translated the codon ACC for residues 394 a R;Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wyn Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A;Title: Human type VII collagen: cDNA cloning and chromosomal A;Reference number: S16316; MUID:91334380; PMID:1871109
A;Accession: S16316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S. Biochem. Biophys. Res. Commun. 183, 958-963, 1992 A;Title: Molecular cloning and characterization of type A;Reference number: PH0844; MUID:92231902; PMID:1567409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Christiano, A.M.; Greenspan, D.S.; Lee, S., J. Biol. Chem. 269, 20256-20262, 1994
A;Title: Cloning of human type VII collagen. A;Reference number: A54849; MUID:94327588; P. A;Accession: A54849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
A54849
A;Experimental source: keratinocyte R;Gammon, W.R.; Abernethy, M.L.; Pac J. Invest. Dermatol. 99, 691-696, 19
                                                                                                                                                                                                                                                                                                                                       A;MOLECULE type: mRNA
A;MOLECULE : 'EFR', 340-475,'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG',524-528,'C'
A;Cross-references: UNIPARC:UPI000017A139; DDBJ:D11152; DDBJ:D13694; NID:g453698; PIDN:
A;Experimental source: keratinocyte
A;Experimental source: keratinocyte
                                                                              A; Residues: 815-892, 'E', 894-1439 < PAR>A; Cross-references: UNIPARC: UPI000016A722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-2944 <CHR>
A;Cross-references: UNIPROT:Q02388; UNIPARC:UPI000017A138; GB:L02870; NID:g987124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collagen alpha 1 (VII) chain precursor -
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                                                                                                                                            ;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGGACGTGGATGACCTGCACATCATTGTCCAAGAGCTGAGGGGCTCCATT 531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValGluAspGluLeuArgGluIleAlaSerGluProValAlaGluHisTyrPheTyrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaAlaLysLysAlaLysAspLeuGlyPheLysMetPheAlaValGlyValGlyAsnAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyAlaAlaLeuLysTyrLeuIleAspAsnSerPheThrValSerSerGlyAlaArgPro
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                             M.L.; Padilla,
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                                                                                 GB:M65158; GB:S49017; NID:g180914; PIDN:AAA9
                                Prisayanh, P.S.;
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                                                                                                                                                                                                                                                                                                          394 and 397
                                                                                                                                                                                                                                                                                  Wynn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           collagen cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence of the alphai(VII
                                                                                                                                                                                                                           mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-Jul-2004
                             Cook, M.E.; Wright,
                                                                                                                                                                                                                                                                                     K.C.;
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F;[7-125]/Domain: amino-terminal nonhelical #status predicted F;36-201/Domain: von Willebrand factor type A repeat homology F;33-318/Domain: fibronectin type III repeat homology <FN1>F;327-413/Domain: fibronectin type III repeat homology <FN2>F;414-502/Domain: fibronectin type III repeat homology <FN3>F;508-593/Domain: fibronectin type III repeat homology <FN4>F;508-593/Domain: fibronectin type III repeat homology <FN4>F;508-693/Domain: fibronectin type III repeat homology <FN5>F;686-771/Domain: fibronectin type III repeat homology <FN5>F;776-862/Domain: fibronectin type III repeat homology <FN5>F;864-952/Domain: fibronectin type III repeat homology <FN7>F;864-952/Domain: fibronectin type III repeat homology <FN8-P;864-952/Domain: fibronectin type III repeat homology <FN8-P;8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: GDB:COL7A1; EBR1; EBD1; EB
A;Cross-references: GDB:128750; OMIM:120120
A;Map position: 3p21.3-3p21.3
A;Note: defects in this gene can result in dominant and recessive dystrophic A;Note: there are 118 introns
C;Complex: type VII collagen is probably a homotrimer
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;954-1045/Domain: fibronectin type III repeat hom F;1052-1219/Domain: von Willebrand factor type A r F;1170-1172/Region: cell attachment (R-G-D) motif F;1189-1253/Region: cysteine/proline-rich F;1254-2783/Region: interrupted helical F;1334-1336/Region: cell attachment (R-G-D) motif F;2553-2555/Region: cell attachment (R-G-D) motif F;2553-2555/
F;2625,2631/binurny -
F;2634,2802,2804/Disulfide
                                                                                                              F;2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>F;2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BFI>F;3877,786,1109/Binding site: status predicted (Asn) (covalent) #status predicted F;2167,2176,2185,2188,2664,2667,2673/Modified site: 4-hydroxyproline (Pro) F;2625,2631/Modified site: 5-hydroxylysine (Lys) #status experimental F;2625,2631/Binding site: carbohydrate (Lys) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: structural component of extracellular polymer associated C;Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxyly; F;1-16/Domain: signal sequence #status predicted <SIGs F;17-2944/product: collagen alpha 1(VII) chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: I48103; MUID:93271985; PMID:8499916
A;Accession: I84686
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A; Residues: 'EFR', 372-517, 'DV', 520-540, 'W', 542-1255 < RES>
A; Residues: 'EFR', 372-517, 'DV', 520-540, 'W', 542-1255 < RES>
A; Cross-references: UNIPARC: UPI000016B3AC; GB: S51236; NID: g262308; R; Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, J. Biol. Chem. 264, 3822-3826, 1989
J. Biol. Chem. 264, 3822-3826, 1989
A; Title: Cleavage of type VII collagen by interstitial collagenase A; Reference number: A30296; MUID: 89139437; PMID: 2537292
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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 'A',1240-1246'G',1248-1250,'XE',1253-1255,'Q',1257,'E';2032,'C',2034-2041;''
A;Cross-references: UNIPARC:UPI000017A13A; UNIPARC:UPI000017A13B; UNIPARC:UPI000017A13C;
A;Cross-references: UNIPARC:UPI000017A13C;
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Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A;Title: Dominant dystrophic epidermolysis bullosa: identification
A;Reference number: A55255; MUID:94224777; PMID:8170945
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A; Residues: 2395-2871, 'S', 2873-2944 <RE2>
A; Cross-references: UNIPARC: UPI000016A724;
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A;Accession: I56328
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Alignment Scores:

No.:

1.92e-10 227.50

Length: Matches:

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A;Molecule type: mRNA
A;Residues: 224-2871 &BON>
A;Residues: 224-2871 &BON>
A;Coss-references: UNIPARC:UPI0000173C38; GB:M24282
A;Note: the authors translated the codon TTC for residue 19
R;Bonaldo, P.; Colombatti, A.
J. Biol. Chem. 264, 20235-20239, 1989
A;Title: The carboxyl terminus of the chicken alpha3 chain
A;Reference number: A32674; MUID:90062147; PMID:2584214
A;Accession: A32674
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A37797
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                  R;Bonaldo, P.; Russo, V.; Bucciotti, F.; Doliana, R.; Colombatti, Biochemistry 29, 1245-1254, 1990
Biochemistry 2014 and functional features of the alpha3 chain in A;Reference number: A34270; MUID:90212613; PMID:2322559
                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-253;312-321;434-453;504-518;635-655;704-717;832-853 <DOL>
A;Cross-references: UNIPROT:P15989; UNIPARC:UP10000173C31; UNIPARC:UP10000173C32;
                                                                                                                                                                                                                                                                                                                                                                                                                                         collagen alpha 3(VI) chain precursor - C;Species: Gallus gallus (chicken)
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216.50
48.0%
33.5%
20.6%
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F;239-404/Domain: von Willebrand factor type A repeat homology < VW02>
F;442-607/Domain: von Willebrand factor type A repeat homology < VW03>
F;642-807/Domain: von Willebrand factor type A repeat homology < VW04>
F;840-1004/Domain: von Willebrand factor type A repeat homology < VW04>
F;840-1004/Domain: von Willebrand factor type A repeat homology < VW05>
F;1033-1197/Domain: von Willebrand factor type A repeat homology < VW05>
F;1033-1197/Domain: von Willebrand factor type A repeat homology < VW07>
F;1439-1604/Domain: von Willebrand factor type A repeat homology < VW07>
F;1639-1804/Domain: von Willebrand factor type A repeat homology < VW09>
F;1639-2101/Domain: von Willebrand factor type A repeat homology < VW09>
F;2043-2379/Domain: collagenous #status predicted < COL>
F;2043-2379/Domain: cell attachment (R-G-D) motif
F;2153-2155/Region: cell attachment (R-G-D) motif
F;2159-2161/Region: cell attachment (R-G-D) motif
F;2079-3137/Domain: non-collagenous #status predicted < CNC>
F;2632-2806/Domain: non-collagenous #status predicted < CNC>
F;2632-2806/Domain: von Willebrand factor type A repeat homology < VW11>
F;2632-2806/Domain: platelet glycoprotein Ib-like #status predicted < GPI>
F;201,2084/2436,2563,2581,2683,2867,2920,3003/Binding site: carbohydrate (Asn) (cov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Intron8: 30/1; 236/1; 437/1; 630/1; 030/1.
C; Superfamily: collagen VI
C; Superfamily: collagen VI
C; Keywords: alternative splicing; cell binding; coiled coil; connective tissue; extracel
C; Keywords: alternative splicing; cell binding; coiled coil; connective tissue; extracel
F; 1-25/Domain: signal sequence #status predicted <SIG>
F; 26-3137/Product: collagen alpha 3(VI) chain #status predicted <NNC>
F; 26-3012/Domain: non-collagenous #status predicted <NNC>
F; 36-202/Domain: von Willebrand factor type A repeat homology <VW01>
F; 36-202/Domain: von Willebrand factor type A repeat homology <VW02>
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A;Cross-references: UNIPARC:UPI0000173C39; UNIPARC:UPI0000173C3A; GB:M24282
C;Genetics:
                              (covalent
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US-10-699-035A-1 (1-537) x A37797 (1-3137)

Gaps: Mismatches: Indels: Conservative:

Length: Matches:

uPhe 197	178 AspAlaValGluGlyGluLeuLysGluIleAlaSerArgProPheAspThrHisLeuPhe 197	Дb
G 474	418 CGAGGCAACTTCCTGGAGCTGTCAGCCGCTGCCTGAGCCCCTGCCGAGAAGCACCTG 474	γQ
lGln 177	158 AlaLeuProSerSerValLeuLysSerAlaHisValAsnMetIleAlaValGlyValGln 177	Db
CGGC 417	358 GGCCCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGC 417	γQ
pval 157	138 SerGluGlyValProGlnValIleIleValLeuThrAspGlyGlnSerGlnAspAspVal	Db
TGTG 357	301CCAGGGGTGCCCAAAGTGCTGGTGTGGGTGACAGATGGCGGCTCCAGCGACCCTGTG	Qy
gAla 137	118 GlyLysGlyLeuGluTyrLeuIleGluAsnHisLeuThrLysAlaAlaGlySerArgAla 137	DЬ
G 300	244 GGCCTGGCGCTGGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGG 300	γQ
sThr 117	98 AsnGlnAspValLeuSerHisIleAlaAsnMetProTyrMetGlyGlyGlySerLysThr	DЬ
CACT 243	184 GGTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGGCGCATGGGTGACACCCCACACT	γQ
oSer 97	78 AlaLeuValGlnPheSerGlyAsnProHisThrGluPheGlnLeuAsnThrTyrPr	Db
CTCG 183	124 AGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGCTCG 18	γQ
gPhe 77	58 ArgGluPheLeuTyrAspValValLysAlaLeuAspValGlyGlyAsnAspPheArgPhe 77	Db
TGCC 123	64 CGGGAGTTTGTGGGGCACCTGGTGCCTCCACTGCCCCTGGGGCACCGGGGCCCTGCGTGCC 123	δ
uVal 57	38 AspIleIlePheLeuValAspSerSerTrpSerIleGlyLysGluHisPheGlnLeuVal	Dъ
GGTT 63	TCAGCCA	Ş

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C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46488
R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
Submitted to the Protein Sequence Database, January 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;MOJecule type: mRNA
A;Residues: 1-741 <AAA>
A;Cross-references: UNIFROT:QBNDE6; UNIPARC:UPI000016ACCB; EMBL:AL137638
A;Experimental source: adult testis; clone DKFZP434J065
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                               ATT
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|AspLeuValPheValIleAspGlySerLysSerLeuGlyGluGluAsnPheGluValVal
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RESULT

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polypeptide

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human

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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 574-585;965-973,'X',975-976;1306-1325;1361-1377;1381-1401;1473-1506,'X',1508
A;Residues: 574-585;9618-9037;2374-2410;2445-2459;2466-2469,'X',2471-2474;2504-2508,'X',
A;Cross-references: UNIPARC:UPI0000173C15; UNIPARC:UPI0000173C16; UNIPARC:UPI0000173C17;
C1C; UNIPARC:UPI0000173C1D; UNIPARC:UPI0000173C16; UNIPARC:UPI0000173C17
[10000173C25; UNIPARC:UPI0000173C26; UNIPARC:UPI0000173C17
R;Zamussi, S.; Doliana, R.; Segat, D.; Bonaldo, P.; Colombatti, A.
J. Biol. Chem. 267, 24082-24089, 192
A;Title: The human type VI collagen gene. mRNA and protein variants of the alpha3 chain
A;Reference number: $28776; MUID:93054780; PMID:1339440
A;Residues: 310-28 <ZAN>
A;Cross-references: UNIPARC:UPI0000173C28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: the mRNA portion of the sequence corresponds to restrace *** *** *** R;Chu, M.L.; Conway, D.; Pan, T.; Baldwin, C.; Mann, K.; Deutzmann, R.; Timpl, R. J. Biol. Chem. 263, 18601-18606, 1988
A;Title: Amino acid sequence of the triple-helical domain of human collagen type A;Reference number: A31952; MUID:89066644; PMID:3198591
                                                                                                                                                                                                                                                                                                                             R;Weil, D.; Mattei, M.G.; Passage, E.; Van Cong, N.; Pribula-Conway, E.am. J. Hum. Genet. 42, 435-445, 1988
A;Title: Cloning and chromosomal localization of human genes encoding A;Reference number: A29848; MUID:88161046; PMID:3348212
A;Accession: C29848
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A;Residues: 2038-2373 <CH4>
A;Residues: 2038-2373 <CH4>
A;Cross-references: UNIPARC:UPI0000173C2E; GB:J04211; GB:M20778
A;Note: parts of the generate were determined by protein sequencing A;Note: parts of the generation of t
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A;Cross-references: UNIPARC:UPI0000173C28; GB:S49432; NID:g260296; PIDN:AAB24261.1; A;Cross-references: UNIPARC:UPI0000173C28; GB:S49432; NID:g260296; PIDN:AAB24261.1; R;Chu, M.L.; Mann, K.; Deutzmann, R.; Pribula-Conway, D.; Hsu-Chen, C.C.; Bernard, MEur. J. Blochem. 168, 309-317, 1987

Eur. J. Blochem. 168, 309-317, 1987

A;Title: Characterization of three constituent Chains of collagen type VI by peptide A;Reference number: S00126; MUID:88029444; PMID:3665927

A;Accession: S00245
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A;Residues: 1-30,237-313,'CWW',318-322,'AR',326-1815,'FD',1818-1819,'ID',1822-3176
A;Cross-references: UNIPARC:UPI0000173C14; EMBL:X52022; NID:g3127925
A;Accession: S24465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Contains: collagen alpha 3(VI) chain, splice form A9/N10(-) (;Species: Homo sapiens (man) (C;Date: 21-Nov-193) #sequence revision 12-Nov-1999 #text change 16-Aug-2004 C;Accession: A59140; S13679; S24465; A57083; S28776; S00245; C31952; C29848; R;Chu, M.L.
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A;Residues: 2024-2046;2092-2156,'R';2203-2208,'X',2210-2211,'X',2213-2227;2228-2251;2314
A;Cross-references: UNIPARC:UPI000016A705; UNIPARC:UPI0000173C29; UNIPARC:UPI0000173C2A;
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           Eur. J. Biochem.
                                                   R;Jander,
                                                              A;Cross-references: UNIPARC:UPI000016A720; GB:M27449; NID:g291919; A;Note: part of this sequence was determined by protein sequencing R;Jander, R.; Rautenberg, J.; Glanville, R.W.
                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 2092-2151 <WEI>
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R.; Rautenberg, J.; Glanville, siochem. 133, 39-46, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-3176 <CHU>
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m A9/N10(-)
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F;2040-2042/Region: cell attachment (R-G-D) motif
F;2136-2138/Region: cell attachment (R-G-D) motif
F;2136-2138/Region: cell attachment (R-G-D) motif
F;2148-2150/Region: cell attachment (R-G-D) motif
F;2154-2156/Region: cell attachment (R-G-D) motif
F;2370-2372/Region: cell attachment (R-G-D) motif
F;2370-2372/Domain: von Willebrand factor type A repeat homology <VW11>
F;2400-2571/Domain: von Willebrand factor type A repeat homology <VW12>
F;2617-2800/Domain: von Willebrand factor type A repeat homology <VW12>
F;2665-2986/Region: alanine/lysine/proline/threonine/valine-rich repeats
F;2987-3072/Domain: alaninal Kunitz-type III repeat homology <FN3>
F;3111-3161/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>F;3111-3161/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>F;36/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status
F;2087/Displayals,2558,2677,2861,3036/Binding site: carbohydrate (Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;26-3176/Product: collagen alpha 3(VI) Chain #status predicted <MAT1>
F;26-2037/Domain: maino-terminal nonhelical #status predicted <ANH>
F;26-30,37-3176/Product: collagen alpha 3(VI) chain, splice form A9/N10(-);
F;26-30,237-3176/Product: collagen alpha 3(VI) chain, splice form A9/N10(-);
F;37-203/Domain: von willebrand factor type A repeat homology <VW01>
F;240-405/Domain: von willebrand factor type A repeat homology <VW02>
F;443-608/Domain: von willebrand factor type A repeat homology <VW04>
F;437-802/Domain: von willebrand factor type A repeat homology <VW05>
F;835-99/Domain: von willebrand factor type A repeat homology <VW07>
F;835-99/Domain: von willebrand factor type A repeat homology <VW07>
F;1031-1394/Domain: von willebrand factor type A repeat homology <VW08>
F;1031-1394/Domain: von willebrand factor type A repeat homology <VW08>
F;1037-1802/Domain: von willebrand factor type A repeat homology <VW08>
F;1037-1802/Domain: von willebrand factor type A repeat homology <VW09>
F;1036-2005/Domain: von willebrand factor type A repeat homology <VW09>
F;1038-2373/Region: interrupted helical
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A;Note: engineered sequence to allow isolation of the Kunitz-type proteinase inhibitor R;Arnoux, B.; Merigeau, K.; Saludjian, P.; Norris, F.; Norris, K.; Bjorn, S.; Olsen, O. submitted to the Brookhaven Protein Data Bank, August 1994
A;Reference number: A52812; PDB:1KNT
A;Reference number: A52812; PDB:1KNT
A;Contents: annotation; X-ray crystallography, 1.6 angstroms, residues 3106-3160
A;Note: engineered sequence expressed in Saccharomyces cerevisiae strain mt-663
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit sines are 5-hydroxylated and subsequently O-glycosylated.
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A;Note: this sequence cannot be reliably placed and probably represents the results f
R;Mayer, U; Poeschl, E; Nischt, R; Specks, U; Pan, T.C.; Chu, M.L.; Timpl, R.
Eur. J. Biochem. 225, 573-580, 1994
B;Title: Recombinant expression and properties of the Kunitz-type protease-inhibitor
A;Reference number: S48709; MUID:95045506; PMID:7525281
A;Accession: S48709
                                                                                                                                                                                                                                              F;2087/Disulfide bonds: interchain #status predicted
F;2007/Disulfide bonds: interchain #status predicted
F;2100,2206,2239,2316,2319/Modified site: 4-hydroxyproline (Pro) #status experimental
F;2103,2209,2212,2322,2337/Binding site: carbohydrate (Lys) (covalent) #status experimental
F;2103,2209,2212,2322,2337/Modified site: 5-hydroxylysine (Lys) #status experimental
F;3111-3161,3120-3144,3136-3157/Disulfide bonds: #status predicted
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C;Complex: type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA) sociations among trimer amino- and carboxyl-terminal domains (with disulfide bonds).
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A; Residues: 'MRAWIFFLLCLAGRALAA', 3102-3176 < MAY>
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                                        Local Similarity:
7.55e-09
207.50
47.4%
31.4%
19.8%
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Matches:
Conservative:
                                        Mismatches:
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R;Kern, A.; Briesewitz, R.; Bank, I.; Marcantonio, E.E. J. Biol. Chem. 269, 22811-22816, 1994
A;Title: The role of the I domain in ligand binding of the A;Reference number: A55348; MUID:94357930; PMID:7521332
A;Accession: A55348
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C;Species: Gallus gallus (chicken)
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995
C;Accession: A55348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-272 <KER>
A;Residues: 1-272 <KER>
A;Cross-references: UNIPROT:O42094; UNIPARC:UPI000017A14E; GB:U10114
F;55-230/Domain: von Willebrand factor type A repeat homology <VWA2>
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type XII collagen alpha-1 chain - eastern newt (fragment)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51027
R;Wei_Y:; Yang, E.V.; Klatt, K.P.; Tassava, R.A.
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Dev. Biol. 168, 503-513,
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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A; Residues: 1-929 <WEI>
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                                     AGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCCTTCGGCCAGCACAGCTCG
                                                                        ArgAsnPheIleSerArgValValGluValPheAspIleGlySerAspArgValGlnIle
                                                                                                               CGGGAGTTTGTGGGGCAGCTGGTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGTGCC
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AlaValSerGlnTyrSerGlyAspProArgThrGluTrpGlnLeuAsnThrHisLysThr
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503-513, 1995
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c;Species: Homo sapiens (man)
c;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change
c;Accession: A45226
R;Briesewitz, R; Epstein, M.R.; Marcantonio, E.E.
J. Biol. Chem. 268, 2989-2996, 1993
A;Title: Expression of native and truncated forms of the human i
A;Reference number: A45226; MUID:93155124; PMID:8428973
A;Accession: A45226
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A;Experimental source: hepatoblastoma cell line Hep62
A;Note: sequence extracted from NGH backbone (NCBH:124326)
F;142-317/Domain: von Willebrand factor type A repeat homology <VWAl>
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                                                                                                                                                                                                                                                                                                     AspIleValIleValLeuAspGlySerAsnSerIle-----TyrProTrpAspSerVal 161
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                                     ACTGGCCTGGCGCTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGG
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F;165-246/Domain: fibronectin type III repeat homology <FN3A>
F;255-338/Domain: fibronectin type III repeat homology <FN3B>
F;347-427/Domain: fibronectin type III repeat homology <FN3C>
F;347-427/Domain: fibronectin type III repeat homology <FN3D>
F;436-S20/Domain: fibronectin type III repeat homology <FN3F>
F;547-632/Domain: fibronectin type III repeat homology <FN3F>
F;641-723/Domain: fibronectin type III repeat homology <FN3F>
F;731-818/Domain: fibronectin type III repeat homology <FN3F>
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A;Title: Undulin is a novel member of the fibronectin-tenascin family of extracellular A;Reference number: A40970; MUID:91373351; PMID:1716629
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A; Residues: 1-843 < JUS>
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C; Accession: A40970
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                                                                             LysProGluAlaGlySerArgThrGlyValSerLysIleGlyIleLeuIleThrAspGly
                                                                                                                  GCTGAAGCATCAGGTGCCCGGCCAGGGGTGCCCAAAGTGCTGGTGTGGGTGACAGATGGC
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                                                                                                                                                     TyrLysGlyGlyAsnThrLeuThrGlyLeuAlaLeuAsnTyrIlePheGluAsnSerPhe
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Search completed: February 13, Job time: 32.438 secs 2006, 13:41:21

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Result
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-MODEL-frame+ n2p.model -DEV=xlp
-Q=/abss/ABSSWEB spool/US10699035/runat 13022006_062441_25416/app_query.fasta_1
-Q=/abss/ABSSWEB spool/US10699035/runat 13022006_062441_25416/app_query.fasta_1
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINNATCH=0.1 -LOOPCL=0 -LOOPEXY=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10699035_@CGN 1 1 580 @runat 13022006 062441 25416 -NCPU=6 -ICPU=3
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EMBL; BC059409; AAH59409.1; -; mRNA.
EMBL; BC059409; AAH59409.1; -; Genomic DNA.
EMBL; AL391244; CA122657.1; -; Genomic DNA.
Ensembl; ENSG00000179403; Homo sapiens.
InterPro; IPR003961; FN III.
InterPro; IPR002035; VWF_A.
Pfam; PP00041; fn3; 2.
Pfam; PP00041; fn3; 2.
Pfam; PP00092; VWA; 1.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00060; FN3; 2.
SMART; SM00037; VWA; 1.
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RC Mammary tumor metastatized to lung. Tumor arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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"Generation and initial analysis of more than 15,000 full-length human
and mouse CDNA sequences.";
RI Proc. Marl. Acad Sci II c a oo.1cool 1col10001
  RC STRAIN-C57BL/JJ; TISSUE-Ovary and uterus;

RX MEDLINE-21085660; PubMed-11217851; DOI-10.1038/35055500;

RA MEDLINE-21085660; PubMed-11217851; DOI-10.1038/35055500;

RA Mara A., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arzakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Niahi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Okazaki Y., Gojobori T., Bono H., Kagukawa T., Saito R.,

RA Aizawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

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RA Shrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Shrimi L.M., Staubli F., Suzuki R., Tomita M., Baldarelli R., Barsh G.,

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RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Czech II;
TISSUE=Mammary tumor
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
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full-length
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; DOI=10.1016/S0076-6879(99)03004-9;
  mouse
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RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;

RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Sumi N., Ishii Y., Nakamura K., Nishine T., Tashivo H., Itoh M.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

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RT "RIKEN integrated sequence analysis (RISA) system-384-format

RT sequencing pipeline with 384 multicapillary sequencer.";

UN [8]

UN [8]
                                                           Pred. No.:
                            Alignment
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A Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
A Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
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Sasaki D., Shibata K., Shinagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.

STRAIN-FVB/N; TISSUE=Colon;

STRAIN-FVB/N; TISSUE=Colon;

Director MGC Project;

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ da

EMBL; BC026919; AAH26919.1; -; mRNA.

EMBL; BC026165; AAH36166.1; -; mRNA.

EMBL; BC036166; AAH36166.1; -; mRNA.

HSSP; P18614; 1MHP

Ensembl; ENSWISG00000042116; Mus musculus.
                                                                       PRINTS; PRO0453; VWFADOMAIN
SMART; SM00060; FN3; 2.
SMART; SM000327; VWFA; 2.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
                                                                                                                                          MGI; MGI:2179729; Vwal.
GO; GO:0005615; C:extracellular
InterPro; IPR003961; FN III.
InterPro; IPR002035; VWF_A.
Pfam; PF00041; fn3; 2.
Pfam; PF00092; VWA; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sanciation updat
Von Willebrand factor A-related protein.
Name=Vwa1; Synonyms=4932416A11Rik, Warp;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                        Q923K3
Q923K3;
                                                                                              of extracellular matrix proteins."; FEBS Lett. 517:61-66 (2002). EMBL, AV303094; AAX38350.1; -; mRNA HSSP; P18614; 1MHP.
   InterPro;
InterPro;
                                               MEDLINE=22057805; Pour Fitzgerald J., Ting
                                                                                                                                                                                                                                      Mammalia; Eutheria;
Muroidea; Muridae;
NCBI_TaxID=10090;
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna
                                                                                Ensembl;
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                                 GO:0005615;
                                               MGI:2179729; 4932416A11Rik.
MGI:2179729; Vwa1.
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                                                                                                                                                            erald J., Ting S.T., Bateman J.F.; a new member of the von Willebrand
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Local Similarity:
                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4932416All product:VON WILLEBRAND FACTOR A-RELATED
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                                                                                           Mus musculus (Mouse).
Bukaryota; Metazoa; Chaniata
Mammalia; Butheria; Euarchontoglires;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                    Name=Vwa1; Synonyms=4932416A11Rik;
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library, clone:4
PROTEIN homolog.
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QBC0Q7;
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SM00327; VWA; 1.
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RX KREDLINE=21085660; PubMed=11217851; DOI=10.1038/35055000; RX KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Adachi J., Fukuda S., RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R., RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Kachi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Ra Blake J., Boffelli D., Hofmann M., Carninci P., de Bonaldo M.F., RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Ra Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Lee N.H., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., RA Hayashiraki Y.:
STRAIN=C57BL/6J; TISSUE=Testis;
Adachi J., Airawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Airawa K., Akimura T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagaki T., Hiraoka T., Hirozane T., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Kasukawa T., Kondo S., Konno H., Kouda M., Koya S., Konno H., Kouda M., Koya S., Konihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Testis;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

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Nature 420:563-573(2002).
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SWART; SM00060; FN3; 2.
SWART; SM00327; VWA; 1.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50234; VWFA; 1.
SEQUENCE 415 AA; 44681 MW;
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46 RAT
A66 RAT
Q642A6; PRELIMINARY; PRT; 415 AA.
Q642A6;
Q5-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Von Willebrand factor A domain-related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005615; C:extracellular InterPro; IPR003961; FN III. InterPro; IPR003935; VWF_A. Pfam; PF00041; En3; 2. Pfam; PF00092; VWA; 1.
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MGI:2179729; Vwal.
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"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC081983; AAH81983.1; -; mRNA.
InterPro; IPR003961; FN III.
InterPro; IPR002035; VWF A.
Pfam; PF00041; fn3; 2.
Pfam; PF00092; VWA; 1.
PRINTS; PR00453.
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PROSITE; PS50234; VWFA; 1.
SEOUENCE 415 AA; 44832
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SMART; SM00060; FN3; 2.
SMART; SM00327; VWA; 1.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna
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13-SEP-2005
13-SEP-2005
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NUCLEOTIDE SEQUENCE.

Genoscope; Whitehead Institute Centre for Genome Research; Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an incomplete the complete the complete that is the complete that the complete the complete that is the complete that the complete that is the complete that the complete t
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I

Actinopterygii; Neopterygii; Teleostei; Buteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodo

Tetradontoidea; Tetraodontidae; Tetraodon.
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13-SEP-2005 (TrEMBLrel. 31,
Chromosome undetermined SCAH
ORFNames=GSTENG00020556001;
                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 431:946-957(2004).
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31, Last sequence update)
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SCAF14659, whole genome sho
                                                                                                                                                                                                                                                                                                                                                    -; Genomic DNA.
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A Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N., And Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Anicaud S., Jaffe D., Fisher S., Luffalla G., Dossat C., Segurens B., An Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Anthouard V., Skalli Z., Cattolico L., Poulain J., De Berardinis V., And Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., And Cruaud C., Lardier G., Chapple C., McKernan K.J., McBwan P., Bosak S., Andrew G., Lardier G., Chapple C., McKernan K.J., McBwan P., Bosak S., Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Kelnibad-Tok K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Allaudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype.";
NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
Genoscope; Whitehead Institute Centre for Genome Research Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an -!- CAUTION: The Number of the EMBL/GenBank/DDBJ entry with the control of the Caution (MGS) entry with the control of the Caution (MGS) entry with the control of the Caution (MGS) entry with the caution (MGS) entry with the caution of the Caution (
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleosto
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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13-SEP-2005 (TYEMBLIRE). 31, Last sequence update)
13-SEP-2005 (TYEMBLIRE). 31, Last annotation update)
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InterPro; IPR003961; FN III.
InterPro; IPR003129; Laminin G TSP
InterPro; IPR001220; Lectin legB.
InterPro; IPR002035; VWF A.
Pfam; PF001391; Collagen; 2.
Pfam; PF00041; fn3; 8.
Pfam; PF00092; VWA; 3.
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SWART; SM00060; FN3; 9.
SWART; SM00210; TSPN; 1.
SWART; SM00327; VWA; 3.
PROSITE; PS50853; FN3; 9.
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1; CAAE01012445; CAF94689.1; -; Genomic_DNA.
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                                                                                                                                                                                              AsnValAlaAspPheHisLeuMet
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                                                                                                                                                                                                                                                                                                                                                                                                                          ProAlaGlnArgLeuArgAspAlaGlyValGluValPheAlaIleGlyValLysAsnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGAGGC
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Best Local Similarity:
Query Match:
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RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

RA Althouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

RA Anthouard V., Jubin C., Castelli V., Roulain J., De Berardinis V.,

RA Parra G., Lardier S., Brottier P., Coutanceau J.P., Gouzy J.,

RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

RA Rellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

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RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahm D., Robinson-Rechavi M.,

RA Lin
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PRINTS; PRO0453; VMFADOMAIN.
SMART; SM00060; FN3; 11.
SMART; SM00307; VWA; 3.
PROSITE; PS50853; FN3; 12.
PROSITE; PS50234; VWFA; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collagen;
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SEQUENCE
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Genoscope; Whitehead Institute Centre for Genome Rese
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databas
-!- CAUTION: The sequence shown here is derived from
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tetraodon nigroviridis (Green puffer).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002035; VWF_A. Pfam; PF00041; fn3; 11. Pfam; PF00092; VWA; 3.
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InterPro; IPR003961; FN III.
InterPro; IPR003962; Fn III. subd.
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ORFNames=GSTENG00020231001;
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Chromosome 14 SCAF14645, whole genome shotgun sequence
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SerLeuValGlnTyrSerArgAspProHisThrGluPheTyrLeuAspSerHisHisAsn
                                                                AGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGCTCG
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P32018; Q6LBLO;
01_JUL_1993 (Rel. 26, 01-OCT-1996 (Rel. 34, 13-SEP-2005 (Rel. 48, 13-SEP-2005 (Rel. 48, 13-SEP-2005 (Rel. 48, 13-SEP-2005)
                                                                                                       Apte S.S.;
Submitted
                                                                                                                                     van der Rest M., Mayne R., Olsen B.K.;
"Cloning of the cDNA for a new member of the class of fibril-
"Cloning of the cDNA with interrupted triple helices.";
associated collagens with interrupted triple helices.";
Eur. J. Biochem. 201:333-338(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                        Collagen alpha 1(XIV)
Name=COL14A1;
  STRUCTURE
                     "Identification and characterization of a heparin binding site within the NC1 domain of chicken collagen XIV."; Matrix Biol. 17:145-149(1998).
                                                            MEDLINE=98357967; PubMed=9694594; Giry-Lozinguez C., Aubert-Foucher
                                                                                    STRUCTURE
                                                                                                                           NUCLEOTIDE SEQUENCE OF 1582-1770.
                                                                                                                                                                             Gordon M., Castagnola P., Dublet B., L
van der Rest M., Mayne R., Olsen B.R.;
                                                                                                                                                                                                  MEDLINE=92037585;
                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE OF 1582-1770.
                                                                                                                                                                                                                                 "Type XIV collagen is a variant of undulin.";
Eur. J. Biochem. 207:549-557(1992).
                                                                                                                                                                                                                                                                 MEDLINE=92339443;
                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE OF 402-1549
                                                                                                                                                                                                                                                                                           Waelchli C., Trueb J., Kessler B., Winterhalter K.H., "Complete primary structure of chicken collagen XIV.", Biochem. 212:483-490(1993).
                                                                                                                                                                                                                                                                                                                 MEDLINE=93185668; PubMed=8444186; Waelchli C., Trueb J., Kessler B.,
                                                                                                                                                                                                                                                                                                                                       TISSUE=Embryo
                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHICK
                                                     der Rest M.;
                                                                                                                                                                                                                                                                                                                                                                      TaxID=9031;
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Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
chain precursor (Undulin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                             DOI=10.1016/S0945-053X(98)90027-0;
E., Penin F., Deleage G., Dublet B.,
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                                                            Penin
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InterPro; IPR008160; Collagen.
InterPro; IPR003961; FN III.
InterPro; IPR002035; VWF A.
Pfam; PP001391; Collagen; 4.
Pfam; PF00041; fn3; 8.
Pfam; PF00092; VWA; 2.
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EMBL; X70792; CAA50063.1; -; m
EMBL; X66138; CAA46928.2; -; m
EMBL; X65122; CAA46288.1; -; m
PMR; A45974; A4597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99280705; PubMed=10350466; DOI=10.1021/bi9900222; Montserret R., Aubert-Foucher E., McLeish M.J., Hill J.M., Jaquinod M., van der Rest M., Deleage G., Penin F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dense connective tissue in skeletal muscle.

PTM: Lysines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in all cases and bind carbohydrates.

PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.

PTM: May contain numerous cysteine residues involved in inter- and intramolecular disulfide bonding.

SIMILARITY: Belongs to the fibril-associated collagens with interrupted helices (FACIT) family.

SIMILARITY: Contains 8 fibronectin type-III domains.

SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s Swiss-Prot entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restuas long as its content is in no way modified and this a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Extracellular matrix. TISSUE SPECIFICITY: Wide tissue distribution; high
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Triple-helical region 2 (COL1)
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Cell attachment site (Potentia
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Signal; Structural prot
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                                                                                                                                                                                                                                                   LT 10
12 TETNG
Q4RP12 TETNG
Q4RP12;
                   Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Verte
Actinopterygii; Neopterygii; Teleostei; Eutel
Acanthomorpha; Acanthopterygii; Percomorpha;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                  13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 10 SCAR15009, whole genome shotgun seque
ORFNames=GSTENG00031322001;
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                                                                   Vertebrata; Euteleostomi;
Euteleostei; Neoteleostei
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                                                Tetraodontiformes;
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P. NUCLBOTIDE SEQUENCE.

A Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

A Jaillon O., Aury J.M., Brunet F., Potit J.L., Stange-Thomann N.,

A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

A Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

A Nicaud S., Jaffe D., Fisher S., Boudet N., Castellano S.,

A Biemont C., Salanoubat M., Levy M., Boudet N., Castellano S.,

A Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

A Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

A Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

A Biemont C., Lardier G., Chapple C., McKernan K.J., McBwan P., Bosak S.,

A Parra G., Lardier G., Chapple C., McKernan K.J., McBwan P., Bosak S.,

A Parra G., Lardier G., Chapple C., McKernan K.J., McBwan P., Bosak S.,

A Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

A Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

A Laudet V., Schachter V., Quetier F., Sauxin W., Scarpelli C.,

Micker P., Lander E.S., Weissenbach J., Roest Crollius H.,

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals

The early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary data.
EMBL; CAAE01015009; CAG09870.1; -; Genomic_DNA.
SEQUENCE 1259 AA; 138606 MW; 844C01B6FE2D0E5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
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|AspValValLeuLeuValAspGlySerTyrSerIleGlyLeuGlnAsnPheAlaLysVal
                                                                                                                                                                                                                                                                                                 GluAspPheAspAlaPheGlnArgIleSerLysGluLeuThrGlnSerIle
                                                                   ---GACGTGGATGACCTGCACATCATTGTCCAAGAGCTGAGGGGCTCCATT
                                                                                                                                                                                                                                     CCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGAGGC
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                                                                                                                 ValArgSerGluLeuGluAlaIleAlaAsnProProAlaAspAsnHisValPheGluVal
                                                                                                                                       AACTTCCTGGAGCTGTCAGCCGCTGCCTGCCGGAGAAGCACCTGCACTTTGTG
                                                                                                                                                                                                          AlaAlaThrAsnLeuArgAsnIleAspValGluIlePheAlaValGlyValLysAspAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCCTGGCGCTGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCA
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rodak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marza M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marza M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MATN4 MOUSE STANDARD; PRT; 6
089029; 089030; Q90WS3;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
10-MAY-2005 (Rel. 47, Last annotation
Matrilin-4 precursor (MAT-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata
Mammalia; Eutheria; Euarchontoglires;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE (ISOFORMS LONG AND SHORT), AND VARIANTS.
STRAIN-C57BL/6J, and CD-1; TISSUE-Fetal;
MEDLINE-98442849; PubMed-9771906; DOI-10.1016/S0014-5793(98)01111-9;
MAGENER R., Kobbe B., Paulsson M.;
                   This Swiss-Prot entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                       human matri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE OF 218-257.
MEDLINE=99043241; PubMed=9827539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Mammary gland;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; Peingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   matrix proteins."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Matn4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wagener R., Kobbe B., Paulsson M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Matrilin-4, a new member of
                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genomic organisation, alternative splicing human matrilin-4.";
                                                                                                    TISSUE SPECIFICITY: Lung, brain, sternum, kidney and hear DEVELOPMENTAL STAGE: The short isoform was detected in 7 mice but not in developing mice (19.5 dpc embryos or in 2 1 days old animals).

SIMILARITY: Contains 4 EGF-like domains.

SIMILARITY: Contains 2 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Major component
                                                                                                                                                                                                           TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                   Name=Short;
                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                               Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lett. 436:123-127(1998).
                                                                                                                                                                                                                                                                       IsoId=089029-1; Sequence=Displayed;
                                                                                                                                                                                                           IsoId=089029-2; Sequence=VSP_001401;
SSUE SPECIFICITY: Lung, brain, stern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                               splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                of the
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    way
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                                                                                                                                                                                                           sternum, kidney and heart.
                                                                                                                                                                                                                                                                                                                                                                                                extracellular matrix
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    There are no modified and
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    this statement
                                            a collaboration
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InterPro; InterPro; InterPro; IPRO020_ InterPro; IPRO020_ Pfam; PPO0008; EGF; 4. Pfam; PP000092; VWA; 2. Pfam; PP00092; VWA; 2. PRINTS; PR00453; VWFADOMĀIN. DR PRINTS; PR00453; VWFADOMĀIN. DR PROSITE; PS00010; ASX HYDROXYL; 2. PROSITE; PS000186; EGF=2; 2. PROSITE; PS50026; EGF=3; FALSE_NF PROSITE; PS50026; EGF=3; Colled college.
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Best Local Similari
                                                                                                                                                                                                                                                                                        Score:
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                                                                                                                                                                            US-10-699-035A-1 (1-537) x MATN4_MOUSE (1-624)
                                                                                                                                                                                                                                                                                                                        Alignment
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VARIANT
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InterPro; IPR000742; EGF 2.
InterPro; IPR006209; EGF_like.
InterPro; IPR011203; Matn_vMA.
InterPro; IPR002035; VWF_A.
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GO; GO:0005615; C:extrac
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                                                                                                                                                                                                                                                                                                                          Scores:
124
                                                                                                                                                                                                                                                    Similarity:
                                 56
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                                                                                                                               GACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTT
                                                               ceedactricedescactrices
                                                                                                      AspLeuValPheMetIleAspSerSerArgSerValArgProPheGluPheGluThrMet
 AGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGCTCG
                               By simil.

By simil.

By similar.

273

By similarity.

284

297

By similarity.

314

By similarity.

9 By similarity.

9 By similarity.

9 By similarity.

9 By similarity.

164

By similarity.

9 By similarity.

9 By similarity.

165

By similarity.

9 By similarity.

167

168

By similarity.

169

Missing (in isoform Short).

/FTId-VSP 001401.

A -> E (in strain C57BL/6J).

G -> D (in strain C57BL/6J).

DFA28D2C94B1A14F CRC64;

**Chess.**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307
221
221
243
262
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265.00
53.4%
36.8%
25.3%
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3; FALSE_NEG
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EGF-like
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mRNA.
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RESULT
COLLATION
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TO DAT 
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COCA1 CHICK STANDARW;
P13944; Q04509;
01-JAN-1990 (Rel. 13, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus ya....
Eukaryota; Metazoa; Chordata, c
Eukaryota; Aves; Neognathae;
                  SPLICING.
TISSUE=Embryo
                                                                                                                      MEDLINE=87317590; PubMed=3476925;
Gordon M.K., Gerecke D.R., Olsen B.R.
"Type XII collagen: distinct extrace!
                                                                                                                                                                                                             "Type XII collagen. A large multidomain to type IX collagen.";
J. Biol. Chem. 264:19772-19778(1989).
                                                                                                                                                                                                                                                                 Gordon M.K., Gerecke D.R., Dublet
                                                                                                                                                                                                                                                                                                          AND
                                                                                                                                                                                                                                                                                                                                                                                         "The complete primary structure of type XII collagen shows a chimeric molecule with reiterated fibronectin type III motifs, von Willebrand factor A motifs, a domain homologous to a noncollagenous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=White leghorn;
MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
Yamagata M., Yamada K.M., Yamada S.S., Shinomura T., Tanaka
Nishida Y., Obara M., Kimata K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
MEDLINE=93042014; PubMed=1420368; DOI=10.1016/0167-4781(92)90145-P;
                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE OF 2456-3124,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                              NUCLEOTIDE SEQUENCE OF 2960-3076.
                                                                                                                                                                                                                                                                                     MEDLINE=90062079; PubMed=2584192;
                                                   NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHICK
                                                                                                                                                                                                                                                                                                                                                          Cell Biol. 115:209-221(1991).
                                                                                                     cDNA cloning
                                                                                                                                                                                                                                                                                                      2846-2873
                                                                                                                                                                                                                                                                                                                                                                                  IX collagen,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGG-----
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                                                                                       Sci.
                                                     QF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - GTGCCCAAAGTGCTGGTGTGGGTGACAGATGGCGGCTCCAGCGACCCT
                                                     1-1283
                                                                                       U.S.A.
                                                                                                                        extracellular matrix component
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; Galliformes; Phasianidae;
                                                     (ISOFORM
                                                                                       84:6040-6044(1987)
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                                                     SHORT),
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                                                     AND
                                                     ALTERNATIVE
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idae; Phasianinae;
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                                                                                                                                                                                                                                                  partial homology
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                    PROSITE; PS50853; FN3; 18. PROSITE; PS50234; VWFA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
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   Alternative
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EMBL; D00824; BAA00701.1; -; ml
EMBL; X61024; CAA43358.1; -; ml
EMBL; M17375; AAA48718.1; -; ml
EMBL; J05137; AAA48635.1; -; ml
EMBL; X67327; CAA47744.1; -; ml
PIR; A40020, A40020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koch M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet "Large and small splice variants of collagen XII: differential expression and ligand binding.", J. Cell Biol. 130:1005-1014(1995).

-!- FUNCTION: Type XII collagen interacts with type I collagen-containing fibrils, the COLI domain could be associated with surface of the fibrils, and the COL2 and NC3 domains may be localized in the perifibrilar matrix.

-!- SUBUNIT: Trimer of identical chains each containing 190 kDa o
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"The two
Biochim.
[5]
PRINTS, PR00453; VWFADOMAIN
SMART; SM00060; FN3; 18.
SMART; SM00210; TSPN; 1.
SMART; SM00327; VWA; 4.
                                                                                            Pfam; PF01391; Collagen; Pfam; PF00041; fn3; 17. Pfam; PF00092; WA; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. use as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95370352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      removed
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                                                                                                                                                                                                                                                                         Ensembl; ENSGALG00000015908;
                                                                                                                                                                                                                                               [nterPro;
                                                                                                                                                                         nterPro;
                                                                                                                                                                                                 nterPro;
                                                                                                                                                                                                                          nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the fibril-associated collagens interrupted helices (FACIT) family.
SIMILARITY: Contains 18 fibronectin type-III domains.
SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
SIMILARITY: Contains 4 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P13944-2; Sequence=VSP_001148; TISSUE SPECIFICITY: Type XII collagen is present in tendons ligaments, perichondrium, and periosteum, all dense connect tissues containing type I collagen.

DOMAIN: This sequence defines five distinct domains, two trest the domains (COL1 and COL2) and three nontriple-helical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2; Comment=The final tissue form of collagen XII may conhomotrimers of either isoform Long or isoform Short combination of isoform Long and isoform Short. Only is a proteoglycan. Isoform Long has more restricted in embryonic tissue than isoform Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: O-glycosylated; glycosaminoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nontriple-helical sequences.
ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Swiss-Prot entry is copyright. It
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                                                                                                                                                                                                                                                                                                        P56199;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prolines at the third position of the tripeptide repeating (G-X-Y) are hydroxylated in some or all of the chains. O-glycosylated; glycosaminoglycan of chondroitin-sulfate t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ins (NC1, NC2, and NC3).
The triple-helical tail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38-Prot entry is copyright. It is produced through the Swiss Institute of Bioinformatics and the Every produced through the Swiss Institute of Bioinformatics.
                                                                                                                                                  IPR003129; Laminin_G_TSP_N.
    IPR002035; VWF_A.
1391; Collagen; 4.
                                                                                                                                                                                                                        IPR008160; Collagen.
IPR003961; FN_III.
                                                                                                                                             Collagen;
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splicing; Cell adhesion; Collagen;

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Best I
Query
DB:
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Best Local Similarity:
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Repeat; Signal; Structural protein.
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          x COCA1_CHICK (1-3124)
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                                                                                                                                      Missing (in isoform

/FTIG=VSP_001148.

T > S (in Ref. 4).

D -> E (in Ref. 2).

P -> A (in Ref. 2).

L -> F (in Ref. 2).

V -> F (in Ref. 2).

QP -> AG (in Ref. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nonhelical region (NC3).
Triple-helical region (C0
imperfection.
Nonhelical region (NC2).
Triple-helical region (C0
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(Potential).
O-linked (Xyl. .
(Potential).
N-linked (GlcNAc
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N-linked
N-linked
N-linked
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Arg/Lys-rich (basic).
N-linked (GlcNAc. .) (Potential O-linked (Xyl. .) (chondroitin (Potential).
O-linked (Xyl. .) (chondroitin
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-> AG (in Ref. 3).
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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ID Q4SH63 T

AC Q4SH63 T

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OS Tetradon

OC Eukaryot

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RN NICLEOTI

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RA Anthouar

RA Biemont

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NUCLEOTIDE SEQUENCE.
Genoscope; Whitehead
Submitted (FEB-2004)
                                                         "Genome duplication
the early vertebrate
                                                                                                                                                                                                                                            NCBI_TaxID=99883;
                                                                                                                                                                                                                                                                                                                                         Chromosome 8
                                                                                                                                                                                                                                                                                                                                                                           Q4SH63;
13-SEP-2005
                                                                                                                                                                                                                                                                                                                                                       13-SEP-2005
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NUCLEOTIDE SEQUENCE.

A Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

MA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

MA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

MA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

MA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

MA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

MA Cruaud C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

MA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

MA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

MA Cruaud C., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

MA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

MA Kellis M., Volff JN., Guigo R., Zoody M.C., Mesirov J.,

MA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Mancker P., Lander E.S., Weissenbach J., Roest Crollius H.,

Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,

Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom.
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostom.
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                       r P., Lander B.S., Weissenbach J., duplication in the teleost fish rly vertebrate proto-karyotype."; 431:946-957(2004).
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(TrEMBLrel. 31, Last sequence up
(TrEMBLrel. 31, Last annotation
8 SCAF14587, whole genome shotgur
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Institute Centre for Genome to the EMBL/GenBank/DDBJ dat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bosak S.,
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RESULT 14
Q5VYK2 HUMAN
Q5VYK2 HUMAN PRELIMINARY;
ID Q5VYK2;
AC Q5VYK2;
DT 01-FEB-2005 (TrEMBLrel. 2)
DT 01-FEB-2005 (TrEMBLrel. 2)
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Query Match:
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SMART; SM00060; FN3; 6.
SMART; SM00210; TSPN 1.
SMART; SM00327; VWA; 2.
PROSITE; PS50853; FN3; 7.
PROSITE; PS50234; VWFA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01391; Collagen; Pfam; PF00041; fn3; 6. Pfam; PF00092; VWA; 2.
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InterPro; IPR003129; Laminin_G_TSP_N
InterPro; IPR002035; VWF_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR008160; Collagen.
InterPro; IPR003961; FN III.
InterPro; IPR003129; Laminin_G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAUTION: The sequence shown here is derived EMBL/GenBank/DDBJ whole genome shotgun (WGS)
                                                                                                            1031 AlaAspTyrGlyGluLeuValAsnIleAlaSerLysProSerAspArgHisValPhePhe 1050
                                                                                                                                                      1011 LysValSerLysGluMetGlnMetAspGlyTyrIleIlePheAlaIleGlyPheAlaAsp
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                                                                                 GTG---GACGTGGATGACCTGCACATCATTGTCCAAGAGCTG 519
                                                                                                                                                                                              ArgGlyValProLysValLeuValValLeuThrAspGlyArgSerGlnAspAspValAsn
                                                                                                                                                                                                                   CCAGGGGTGCCCAAAGTGCTGGTGTGGGTGACAGATGGCGGCTCCAGCGACCCTGTGGGC
                                                                                                                                                                                                                                                                             asnLysGluAlaLeuLeuGluAlaIleGlnLysIleSerTyrLysGlyGlyAsnThrLys
                                                                                                                                                                                                                                                                                                                    ValAlaIleAlaGlnPheSerAspAspAlaArgThrGluPheGlnLeuSerSerHisSer
                                                                                                                                                                                                                                                                                                                                             GCCAGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGC
                                                                                                                                                                                                                                                                                                                                                                               CGGGAGTTTGTGGGGCAGCTGGTTCCACTGCCCCTG----GGCACCGGGGCCCTGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                            GACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTT
                                                                     ThrGlyArgAlaIleLysHisValLysGluSerIlePheSerLeuGluAlaGlyAlaArg
                                                                                                                                                                                                                                                                                                    TCGGGTGAGGCTGCCCAGGATGCGGTGCGTGCCTTCTGCCCAGCGCATGGGTGACACCCAC
                                                                                                                                                                                                                                                                                                                                                                ThrArgPheLeuHisSerThrValGlySerLeuAspLeuIleGlyThrAspGlyThrGln
                                                                                                                                                                                                                                                                                                                                                                                                        AspLeuValPheLeuValAspGlySerTrpSerIleGlyAspGluAsnPheMetLysIle
                                                                                                                                 GGCAACTTCCTGGAGCTGTCAGCCGCTGCCTCAGCCCCTGCCGAGAAGCACCTGCACTTT
                                                                                                                                                                          CCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGA
                                                                                                                                                                                                                                                           ACTGGCCTGGCGCTGGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Extracellular matrix;
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                               PRELIMINARY;
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56.3%
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25.1%
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Created)
Last sequence update)
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Matches:
Conservative:
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US-10-699-035A-1 (1-537) x Q5VYK2_HUMAN (1-2884)
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Best Local Similari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:000578; C:extracellular matrix (sensu Metazoa);
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
GO; GO:0007155; P:phosphate transport; IEA.
InterPro; IPR008160; Collagen.
InterPro; IPR008161; FN III.
InterPro; IPR003129; Laminin G TSP N.
InterPro; IPR002035; VWF A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50853; FN3; 18.
PROSITE; PS50234; VMFA; 4.
Collagen; Extracellular matrix;
SEQUENCE 2884 AA; 315869 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00453; VWFADOMAIN. SMART; SM00060; FN3; 18. SMART; SM00210; TSPN; 1. SMART; SM00327; VWA; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01391; Collagen; Pfam; PF00041; fn3; 18. Pfam; PF00092; VWA; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-2005 (T-EMBLrel. 31, Last annotation Collagen, type XII, alpha 1. Name=COLL2A1; ORFNames=RP1-238D15.1-003; Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
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|AppIleValPheLeuValAspGlySerTyrSerIleGlyIleAlaAsnPheValLysVal
                                                                                                                                         ArgAlaPheLeuGluValLeuValLysSerPheGluIleSerProAsnArgValGlnIle
                                                                      AGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGCTCG
                                                                                                                                                                                                                                                                                                                                                                             GACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTT
SerLeuValGlnTyrSerArgAspProHisThrGluPheThrLeuLysLysPheThrLys
                                                                                                                                                                                                                        CGGGAGTTTGTGGGGCAGCTGGTGGCTCCACTGGCCCCTGGGGCACCGGGGCCCCTGCGTGCC
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1; -; Genomic_DNA.
1; -; Genomic_DNA.
1; JOINED; Genomic_DNA.
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Matches:
Conservative:
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COP715, CO9716;

CO9715, CO9716;

15-JUL-1998 (Rel. 36, 115-JUL-1998 (Rel. 36, 110-MAY-2005 (Rel. 47, 110-MAY-2005 
                                                                                                                                                                                                                                                                                                                                                                                      chromosome 6q12-q13.";
Genomics 41:336-242(1997).
-!- FUNCTION: Type XII collagen interacts with type I collagen-
containing fibrils, the COL1 domain could be associated with
surface of the fibrils, and the COL2 and NC3 domains may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97288521; PubMed=9143499; DOI=10.1006/geno.1997.4638; Gerecke D.R., Olson P.F., Koch M., Knoll J.H.M., Taylor R., Hudson D.L., Champliaud M.-F., Olsen B.R., Burgeson R.E.; "Complete primary structure of two splice variants of collagen and assignment of alpha 1(XII) collagen (COL12A1), alpha 1(IX) collagen (COL12A1), and alpha 1(XIX) collagen (COL19A1) to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collagen alpha 1(XII)
Name=COL12A1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
                                                                                    IsoId=Q99715-2; Sequence=VSP_001149; TISSUE SPECIFICITY: Found in collagen I-containing tissues: both isoform Short and isoform Long appear in amnion, chorion, skeletal muscle, small intestine, and in cell culture of dermal fibroblasts, keratinocytes and endothelial cells. Only the short force.
   PTM:
each
PTM:
                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
Comment=The final tissue form of collagen XII may contain
homotrimers of either isoform Long or isoform Short or an
combination of isoform Long and isoform Short;
                                                                                                                                                                                                                                                                                                                                                      localized in the perifibrillar matrix (By similarity) SUBUNIT: Trimer of identical chains each containing 1
                                                                                                                                                                                       Name=Short
                                                                                                                                                                                                                                                                                                                   nontriple-helical sequences.
ALTERNATIVE PRODUCTS:
                                                         isoform is found in lung, placenta, kidney carcinoma cell line.
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                                                                                                                                                                                                        IsoId=Q99715-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValGluAspIleIleGluAlaIleAsnThrPheProTyrArgGlyGlySerThrAsnThr
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                     The triple-helical tail is stabilized end (By similarity).
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Last annotation update)
chain precursor.
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InterPro; IPRO08160; Collagen.
InterPro; IPRO03961; FN III.
InterPro; IPRO02035; VWF A.
Pfam; PF01391; Collagen; 4.
Pfam; PF00041; fn3; 18.
Pfam; PF00092; VWA; 4.
PRINTS; PR00453; VWFADOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alternative splicing; Cell adhesion; Direct protein sequencing; Extracelladroxylation; Rename
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U73778; AAC51244.1;
EMBL; U73779; AAD40483.1;
HSSP; P18614; 1MHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50853; FN3; 18. PROSITE; PS50234; VWFA; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005595; C:collagen type XII; TA:GO; GO:0001501; P:skeletal development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGNC; HGNC:2188; COL12A1.
MIM; 120320; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chondroitin-sulfate type (By similarity).

SIMILARITY: Belongs to the fibril-associated interrupted helices (FACIT) family.

SIMILARITY: Contains 18 fibronectin type-III SIMILARITY: Contains 1 TSP N-terminal (TSPN) SIMILARITY: Contains 4 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unit (G-X-Y) are hydroxylated in some similarity).

PTM: O-glycosylation of isoform Long;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENSG00000111799; Homo sapiens
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Bioinformatics Institute.
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mRNA.
Hydroxyproline Hydroxyproline
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Cell attachment site (Potential)
Cell attachment site (Potential)
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Triple-helical
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Fibronectin type-III 1.
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Search completed: February 13, 2006, 13:38:53 Job time: 147.574 secs

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GenCore version 5.1.7
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Result
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-Q=/abss/ABSWEB spool/US10699035/runat 13022006 062440 25403/app query.fasta 1
-Q=/abss/ABSSWEB spool/US10699035/runat 13022006 062440 25403/app query.fasta 1
-DB=A Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -L\(\tilde{O}\)PCL=0 -L\(\tilde{O}\)PEXT=0
-UNIT\(\tilde{S}\)=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000000 -HOST=abss02p
-USER=US10699035 @CGN 1 476 @runat 13022006 062440 25403 -NCPU=6 -ICPU=3
-NO_MAAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -L\(\tilde{O}\)CRES=0 -DEV_TIMEOUT=120
-MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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ALIGNMENTS

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02-MAY-2001; 2001AU-00004701.		02-MAY-2002; 2002WO-AU000542.	07-NOV-2002.		WO200288184-A1.		/note= "Encoded by CTC"	Misc-difference 179180	/note= "Encoded by GGG"	Misc-difference 12	Location/Qualifiers	Homo sapiens.	gene therapy; human.	extracellular matrix; ECM; molecular marker; cartilage; arthritis;	Willebrand Factor A domain related-protein; von Willebrand Factor	Human von Willebrand Factor A (VA) domain.	24-MAR-2003 (first entry)		2500;	AAE32500 standard; protein; 180 AA.			

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Bateman JF,

Fitzgerald DJ;

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Percent Similarity:
Best Local Similarity
Query Match:
DB:
                                                                                                                                            Alignment
                                                                                                                                                                            The invention relates to Willebrand Factor A domain related-protein (MARP) which is a member of von Willebrand Factor A (VA)-domain protein superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The present sequence is human VA domain
                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated Willebrand Factor A-Related Protein polypeptide useful for the manufacture of a medicament in the treatment of a disease condition of the extracellular matrix, in particular arthritis.
                                                                                                                                            Sequence 180
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 72-73; 103pp; English.
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Matches:
Conservative:
Mismatches:
Indels:
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á 밁 Ś В á В Ş 밁 US-10-699-035A-1 (1-537) δ В Ś Ś В á 밁 Ś 뫄 181 301 241 121 142 122 102 162 481 421 361 82 62 42 22 1 GGGGACCTGATGTTCCTGCTGGACAGCTCAGCGAGCGTCTCTCACTACGAGTTCTCCCCGG N TCGGGTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCAC 240 ACTGGCCTGGCGCTGGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGG AlaSerLeuValHisValGlySerArgProTyrThrGluPheProPheGlyGlnHisSer GCCAGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGC CCAGGGGTGCCCAAAGTGCTGGTGTGGGTGACAGATGGCGGCTCCAGCGACCCTGTGGGC GGCAACTTCCTGGAGCTGTCAGCCGCTGCCTCAGCCCCTGCCGAGAAGCACCTGCACTTT CCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGA ThrGlyLeuAlaLeuValTyrAlaLysGluGlnLeuPheAlaGluAlaSerGlyAlaArg ValAspValAspAspLeuHisIleIleValGlnGluLeuArgGlySerIleLeu 179 GTGGACGTGGATGACCTGCACATCATTGTCCAAGAGCTGAGGGGCTCCATTCTC 534 GlyAsnPheLeuGluLeuSerAlaAlaAlaSerAlaProAlaGluLysHisLeuHisPhe ProGlyValProLysValLeuValTrpValThrAspGlyGlySerSerAspProValGly x AAE32500 (1-180)101 120 420 41 21 61 480 141 121 300

RESULT 2 AAB87344 ID AAB

AAB87344 standard; protein;

> AAB87344;

22-MAY-2001 (first entry)

Human gene 3 encoded secreted protein HNTEO78, OI DES NO:85

Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification. Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; inflammation;

Homo sapiens.

WO200118022-A1

15-MAR-2001

31-AUG-2000; 2000WO-US024008

03-SEP-1999; 03-SEP-1999; 99US-0152315P. 99US-0152317P.

(HUMA-) HUMAN GENOME SCI INC.

Soppet PA, Baker KP, DR, Young Young Shi Y, Birse CE, Fiscella M, PE, Ebner R, Duan DR, Wei Y, Florence KA; Komatsoulis GA, Rosen CA; Olsen HS, Lafleur DW;

2001-203081/20.

preventing, treating Parkinson's diseases Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and and cancers.

Claim 11; Page 532-533; 607pp; English.

CC AAB9185-AAF91929 represent cDNAs corresponding to 52 human secreted CC protein genes, and AAB87342-AAB87413 represent the proteins they encode. AAB87414-AAB87454 represent human secreted protein fragments. The genes can their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene conductions in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the community of the new protein in a sample or by determining the presence of community of the new genes. Specific uses are described for each of the community of the new genes. Specific uses are described for each of the community of the new genes. Specific uses are described for each of the community of the new genes. Specific uses are described for each of the community of the new genes. Specific uses are described for each of the community of the new genes. Specific uses are described for each of the community of the new genes. Specific uses are described for each of the community of the new genes. Specific uses are described for each of the community of the new genes. Specific uses are described for each of the community of the new genes. Specific disorders, diseases of the immune system, comparison of the proteins of the community developmental comparison of the proteins can also be used to allow ound the community of primary tissues, to regenerate tissues, to dentify their compared to maintain organs before transplantation, for supporting cell community of maintain organs before transplantation, for supporting cell community of maintain organs before transplantation, for supporting cell as a food additive or preservative to modify storage properties.

CC Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and indusposite the invention of the invention engine linked community of the present sequence represents a human general protein of the inventio

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RESULT 3
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AC ABG6
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Query Match:
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                                                                                                       Albumin fusion protein; therapeutic protein X; human albumin; human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder chaematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer;
                                                                                                                                                                                 Human albumin fusion protein #2022.
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                                               Homo sapiens
                                                                                  immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
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25-APR-2000; 2000US-0199384P
21-DEC-2000; 2000US-0256931P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 215
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ValArgGluPheValGlyGlnLeuValAlaProLeuProLeuGlyThrGlyAlaLeuArg
                                                    ACTGGCCTGGCGCTGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGG
                                                                                                         TCGGGTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCAC
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Matches:
Conservative:
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Indels:
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                                                                                       CC The invention relates to a novel albumin fusion protein. The invention CC further relates to: a composition comprising the albumin fusion protein CC and a pharmaceutical carrier; a kit comprising the composition of the CC albumin fusion protein formula; a method of treating a disease or CC disorder in a patient comprising the step of administering the albumin CC fusion protein; a method of treating a patient with a disease or disorder CC that is modulated by Therapeutic protein: X, or its fragment or variant; CC fragment or variant; a nucleic acid molecule comprising a polynucleotide cC fragment or variant; a nucleic acid molecule comprising the protein and a host cell comprising the albumin fusion protein; and a host cell CC comprising the nucleic acid molecule of the albumin fusion protein. The CC comprising the nucleic acid molecule of the albumin fusion protein. The CC comprising the nucleic acid molecule of the albumin fusion protein. The CC comprising the nucleic acid molecule of the following CC cativities: cytostatic, antianaemic, antiarthritic, antiasthmatic, antiasthmatic, antianaemic, dermatological, antigout, immunomodulator, antiarrhythmic, CC cardiant, nootropic, antilipaemic, nephrotropic, uropathic, anabolic, neuroprotective, antiparakinsonian, tranquilizer, antidiabetic, anabolic, hypertensive and uniterary mass lbumin fusion protein and continuous and anabolic, antiparakinsonian, tranquilizer, antidiabetic, anabolic, hypertensive and uniterary mass lbumin fusion protein and continuous and anabolic, antiparakinsonian, tranquilizer, antidiabetic, anabolic, hypertensive and uniterary mass lbumin fusion protein and continuous and uniterary mass lbumin fusion protein anabolic, antiparakinsonian, tranquilizer, antidiabetic, anabolic, anabolic, antiparakinsonian, tranquilizer, antidiabetic, anabolic,
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25-APR-2000;
21-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New albumin fusion proteins, useful for diagnosing, treating, preventing or ameliorating diseases or disorders e.g. cancer, anemia, arthritis, asthma, inflammatory bowel disease or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiasthmatic; anti-HIV; immunosuppressive; antiinflammatory;
antipsoriatic; antibacterial; osteopathic; dermatological; antigout
immunomodulator; antiarrhythmic; cardiant; nootropic; antilipaemic;
hypertensive, and vulnerary. The albumin fusion protein nucleic acid mabe used in gene therapy to treat disorders. The albumin fusion protein useful for diagnosing, treating, preventing or ameliorating diseases or disorders comprising indication: Y. The diseases or disorders include:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-090519/09.
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CC Paget's disease, systemic lupus erythematosus, gout, muscular dystrophy CC or cachexia), cardiocascular disease (e.g. rhabdomyomas, heart disease, carriythmia, cardiocascular disease, e.g. foetal alcohol syndrome, CC arrhythmia, mixed foetal diseases (e.g. foetal alcohol syndrome, CC Down's syndrome, Patau syndrome, Turner's syndrome, Apert syndrome or Tay CC tract infections or renal disorders), neural or sensory disease (e.g. trinary incontinence, urinary tract infections or renal disorders), neural or sensory disease (e.g. Alzheimer's disease, Parkinson's disease, cerebral malaria, meningitis, CC erebellar atxia, attention deficit disorder, autism or obsessive compulsive disorder), respiratory disease (e.g. emphysema, lung cancer or cocupational lung disease), endocrine diseases (e.g. diabetes, Addison's CC disease or glomerulonephritis), digestive diseases (e.g. portal CC hypertension, irritable bowel disease, gastric atrophy or pancreatitis) cor connective tissue or epithelial diseases (e.g. Crohn's disease, cerebrants a therapeutic protein x relating to the albumin fusion protein consider from the Ingero, website
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease), reproductive system disorders (e.g. prostatitis, inguinal hernia, varicocele, penile carcinoma, ovarian adenocarcinoma or Sertoli-leydig tumours), musculoskeletal diseases (e.g. giant cell tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lymphocytic anaemia, multiple myeloma, arthritis, asthma, AIDS, autoimmune disease, inflammatory bowel disease, psoriasis or Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer (e.g. leukaemia, colon, bone, breast, liver or lung cancer), immune or haematopoietic diseases (e.g. anaemia, Hodgkin's disease,
the
website
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Sequence 215 B

Alignment Scores: Pred. No.:

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ValAspVal/	GTGGACGTG	GlyAsnPhel	GGCAACTTC	ProProMetG	CCCCCCATG	ProGlyValP	CCAGGGGTG	ThrGlyLeuA	ACTGGCCTG	SerGlyGluAl	TCGGGTGAG	AlaSerLeu	GCCAGTCTG	ValArgGluPhe	GTTCGGGAG	GlyAspLeuMet	GGGGACCTG	1-1 (1-537)		imilarity:	† ·
AspAspLeuHi	GTGGACGTGGATGACCTGCACATCATTGTCCAAGAGCTGAGGGGCTCCATTCT	LeuGluLeuSerA	GGCAACTTCCTGGAGCTGTCAGCCGCTGCCTCAGCCCCTGCCGAGAAGCACCTGCACTT	linGluLeuLysAspLeuGlyValThrVal	CCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGA	roLysVal	CCAGGGGTGCCCAAAGTGCTGGTGTGGGTGACAGATGGCGGCTCCAGCGACCCTGTGGGC	laLeuVal	rggcgcrggrcra	aA1	TCGGGTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCCAC	aSerLeuValHisValGlySerArgProTyrThrGluPheProPheGl	GCCAGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCCTTCGGCCAGCACAGC	ValG1	TTGTGGGGCA	Phe	GGGGACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTAC	x ADL78614	æ	100.0%	4.68e-69 902.00
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RESULT 5
ADB 7424
ADB
CC AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted CC AAB87414-AAB87454 represent human secreted proteins they encode. CC AAB87414-AAB87454 represent human secreted protein fragments. The genes CC and their corresponding secreted proteins are useful for preventing. CC treating or ameliorating medical conditions, e.g., by protein or gene CC amount of the new genes. Specific uses are described for each of the CS genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of CC and include developing products for the diagnosis or treatment of CC proliferative disorders, cancer, tumours, foetal and developmental call abnormalities, haematopoietic disorders, diseases of the immune system, CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, CC allergies, neurological disorders (e.g., Alzheimer's disease, CC cardiovascular disorders, pregnancy-related disorders, asthma, skin CC disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, CC gastrointestinal disorders, pregnancy-related disorders, endocrine CC disorders, and infections. The proteins can also be used to aid wound the compared properties of primary tissues, to regenerate tissues, to identify their CC cognate ligands or binding partners, and in chemotaxis, and can be used CC as a food additive or preservative to modify storage properties.

CC alleviating symptoms associated with the disorders mentioned above, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preventing, treating or ameliorating Parkinson's diseases and cancers.
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endocrine disorder; infection; wound healing; vulnerary; cell culture;
chemotaxis; food additive; binding partner identification.
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immunosorbent assay (ELISA). The present sequence represents a hum
secreted protein fragment referred to in the disclosure of the inv
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                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                              CC and their corresponding secreted proteins are useful for preventing, cc treating or ameliorating medical conditions, e.g., by protein or gene ct therapy. Pathological conditions can be diagnosed by determining the camount of the new protein in a sample or by determining the preventing to the camount of the new genes. Specific uses are described for each of the CC amount of the new genes. Specific uses are described for each of the CC proliferative disorders, cancer, tumours, foetal and developmental and camourmalities, haematopoietic disorders, diseases of the immune system, cancer, tumours, foetal and developmental CC abnormalities, haematopoietic disorders, diseases of the immune system, callergies, neurological disorders (e.g., Alzheimer's disease, CC parkinsons's disease), cognitive disorders, schizophrenia, asthma, skin CC disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, CC parkinsons's disease), cognitive disorders, kidney disorders, endocrine CC disorders, and infections. The proteins can also be used to aid wound CC thealing and epithelial cell proliferation, to prevent skin aging due to comburn, to maintain organs before transplantation, for supporting cell CC culture of primary tissues, to regenerate tissues, to identify their CC cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

CC Antibodies specific for a protein of the invention can be used in disgnostic immunoassays e.g., radioimmunoassay created above, and cin disgnostic immunoassays e.g., radioimmunoassay entering a human cC secreted protein fragment referred to in the disclosure of the invention
                                                                                                                                                                                                               Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87342-AAB87413 represent the proteins they encode. AAB87414-AAB87454 represent human secreted protein fragments. The genes
                                                                                                                                                                                                                                                                                                                                Sequence
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03-SEP-1999;
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                      GTTCGGGAGTTTGTGGGGCAGCTGGTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGT
                                                          GlyAspLeuMetPheLeuLeuAspSerSerAlaSerValSerHisTyrGluPheSerArg
                                                                            GGGGACCTGATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGG
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11-JAN-2000;
02-MAY-2000;
AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can
                                    which encode human secretory or membrane proteins represented by AAB8 - AAB88419. Included in the invention are primers AAF93917 - AAF94295
                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                             Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes.
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                                                             This invention relates to nucleic acid sequences AAF93744 -
                                                                                                                           Nucleic acids encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The college may be used to study the expression and function of antibodies against them and in assays to identify modulators (agonists and activity. The antibodies and antagonists of expression and activity. The antibodies and antibodies may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme colinked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid arthritis and diabetes
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                                                                                                                                                                                                                                                                                                        Score:
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                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel human secretory proteins or membrane proteins, and their coding sequences. The present sequence is one such protein sequence. The coding sequences of the invention are useful for examination and diagnosis of abnormality of the human secretary proteins and in gene therapy methods. The coding sequences are proteins are useful as candidates for medicines or as target molecules for developing medicines. Antibodies against the proteins of the invention are useful for treating diseases that are associated with the proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained from sequence information supplied by the European Patent Office.
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02-MAY-2000;
07-JUL-2000;
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ACTGGCCTGGCGCTGGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGG
                                     SerGlyGluAlaAlaGlnAspAlaValArgAlaSerAlaGlnArgMetGlyAspThrHis
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                                                   Claim 11;
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (WARP) which is a member of von Willebrand Factor A (VA)-domain protein superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The present sequence is human WARP protein
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                                                   ACTGGCCTGGCGCTGGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGG
                                                                                          TCGGGTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCAC
                                                                                                                                                 CCAGGGGTGCCCAAAGTGCTGGTGTGGGTGACAGATGGCGGCTCCAGCGACCCTGTGGGC
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ProGlyValProLysValLeuValTrpValThrAspGlyGlySerSerAspProValGly

152

GGCAACTTCCTGGAGCTGTCAGCCGCTGCCGCTGCCGCAGAAGCACCTGCACTTT

480 172 420

192

GlyAsnPheLeuGluLeuSerAlaAlaAlaSerAlaProAlaGluLysHisLeuHisPhe

ABP69674

standard;

protein;

(first entry)

Human polypeptide SEQ ID NO 1721.

Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infectional tiple sclerosis; diabetes; genetic disorder; wound; burn; infections; selections; s

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Query
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                                                                                                                                                                                                                                                                                                                                                                                protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cell-proliferative disorders (cancer), neurodegenerative diseases (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid disorders, platelet or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                Local Similarity:
                                                                                                                                                                                                                                                                                                                                                          Sequence 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; SEQ ID NO 1721; 1012pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
                                                                                                                                                                                                                                                                                                           No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleotide sequence selected from any of 948 sequences (ABZ11119-ABZ12066) or their mature protein coding portion, active domain coding
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T, Wang J,
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                                                                                                                                              GlyAspLeuMetPheLeuLeuAspSerSerAlaSerValSerHisTyrGluPheSerArg
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TCGGGTGAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCAC
                    GCCAGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCCTTCGGCCAGCACAGC
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Ma Y, Yamazaki V, Chen R,
, Wang D, Drmanac RT;
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2002US-0385784P

2002US-0386041P

2002US-038604P

2002US-0386376P

2002US-03868649P

2002US-0386869P

2002US-0386816P

2002US-038691P

2002US-038691P

2002US-0386972P

2002US-0386972P

2002US-0387262P

2002US-038735P

2002US-0387400P

2002US-038761P

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09-AUG-2002
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113-AUG-2002

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Smithson G,
Zhong H;
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Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
Paddigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
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                                                                           polypeptides and nucleic acid molecules useful for preventing NOVX-associated disorders, e.g. cancer, diabetes, infection or and in chromosome mapping, tissue typing or pharmacogenomics.
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2002US-0388096P.
2002US-0388002CP.
2002US-038802CP.
2002US-0389122P.
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2002US-0389742P.
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2002US-041682P.
2002US-041683P.
2002US-0411839P.
2002US-0412528P.
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2002US-04123130P.
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AC AAE03
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DE Human

AAE03654

protein;

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cell adhesion molecule-18

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210 534 GlyAsnPheLeuGluLeuSerAlaAlaAlaSerAlaProAlaGluLy8HisLeuHisPhe

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Query Match:
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Conservative:
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inflammatory disorder; acquired immune deficiency syndrome; AIDS; Addison's disease; allergy; anaemia; asthma; atherosclerosis; melanoma; Crohn's disease; diabetes mellitus; asthma; theropic dermatitis; lymphoma; cancer; glomerulonephritis; multiple sclerosis; Grave's disease; osteoarthritis; osteoporosis; psoriasis; rheumatoid arthritis; ulcerative colitis; infection; cell proliferative disorder; actinic keratosis; myeloma; Human; extracellular matrix and cell adhesion molecule; XMAD; gene therapy; genetic disorder; adremoleukodystrophy; leukaemia; Down's syndrome; cystic fibrosis; Gaucher's disease; myotonic dystrophy; sickle cell anaemia; thalassaemia; autoimmune disorder; adenocarcinoma; neuroprotective; dermatological. arteriosclerosis; nootropic; anticonvulsant; antithyroid; nephrotropic;

Homo sapiens

Region Key 'note= "Von Willebrand factor note= Location/Qualifiers note= .170 . 51 "Collagen glycoprotein "Collagen "Collagen glycoprotein precursor" "Collagen glycoprotein glycoprotein precursor" precursor" precursor" domain score"

WO200142285-A2

05-DEC-2000; 2000WO-US032990

10-DEC-1999; 16-DEC-1999; 99US-0172852P 99US-0172354P

INCYTE GENOMICS INC.

Baughn ₩ ₩ Tang . Lu r DAM, Lal P Shah Burford N, Azimzai Y, P, Au-Young J; Au-Young Patterson û

N-PSDB; 2001-381632/40

New human extracellular matrix and cell adhesion molecules and polynucleotide sequences encoding them, useful for diagnosis, prevention, treatment of genetic, autoimmune and cell proliferative disorders.

Claim 1; Page 111; 135pp; English

cc polynucleotides encoding XMAD are useful in somatic or germline gene therapy to correct a genetic deficiency, to express a conditionally clethal gene product and to express a protein which affords protection against intracellular parasites and also for diagnosis of disorders associated with expression of XMAD. They are also used for generating thybridisation probes useful in mapping the naturally occurring genomic sequences and to create knock in humanised animals (pigs) or transgenic animals (mice or rats) to model humanised animals (pigs) or transgenic fragments derived from the polynucleotide sequences may be used as celements on a microarray. Antibodies which specifically bind XMAD may be used for the diagnosis of disorders associated with the expression of the superspector of the control of the superspector of the control of t The present sequence is a human extracellular matrix and cell adhesion molecule (XMAD). The XMAD is used for screening a compound for effectiveness as an agonist or antagonist of XMAD. The identified agonior antagoinst are used for treating a disease or condition associated with decreased or increased expression of functional XMAD. The syndrome (AIDS), Addison's Crohn's disease, disease, diabetes allergies, anaemia, asthma dermatitis agonist

> 밁 Ş 밁 S 밁 Š B δ B Ś 밁 á 밁 Ş 밁 á 밁 ઇ Query Match: DB: Score: **ព័ត្**ពព័ត្តពង្គង្គ US-10-699-035A-1 (1-537) Best Local Percent Similarity: glomerulonephritis, multiple sclerosis, Grave's disease, osteoarthritis, osteoporosis, psoriasis, rheumatoid arthritis, ulcerative colitis, bacterial, fungal, parasitic, protozoal and helminthic infections and cell proliferative disorders such as actinic keratosis, arteriosclerosis and cancer including breast, bladder, bone marrow, brain and uterus Sequence 185 No : 490 430 370 310 Scores: 161 141 121 101 190 130 81 61 Similarity: 41 70 21 10 μ GlnGluLeuLysAspLeuGlyValThrValPheIleValSerThrGlyArgGlyAsnPhe GTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCCTTCGGCCAGCACAGCTCGGGTGAG TTTGTGGGGCAGCTGGTGGCTCCACTGCCCCTGGGGCACCGGGGCCCCTGCGTGCCAGTCTG AspAspLeuHisIleIleValGlnGluLeuArgGlySerIleLeu GATGACCTGCACATCATTGTCCAAGAGCTGAGGGGGCTCCATTCTC ProLysValLeuValTrpValThrAspGlyGlySerSerAspProValGlyProProMet AlaLeuValTyrAlaLysGluGlnLeuPheAlaGluAlaSerGlyAlaArgProGlyVal GCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCCACACTGGCCTG ValHisValGlySerArgProTyrThrGluPheProPheGlyGlnHisSerSerGlyGlu PheValGlyGlnLeuValAlaProLeuProLeuGlyThrGlyAlaLeuArgAlaSerLeu MetPheLeuLeuAspSerSerAlaSerValSerHisTyrGluPheSerArgValArgGlu LeuGluLeuSerAlaAlaAlaSerAlaProAlaGluLysHisLeuHisPheValAspVal CTGGAGCTGTCAGCCGCTGCCTCAGCCCCTGCCGAGAAGCACCTGCACTTTTGTGGACGTG CAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGAGGCAACTTC CCCAAAGTGCTGGTGGGTGACAGATGGCGGCTCCAGCGACCCTGTGGGCCCCCCCATG GCGCTGGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCAGGGGTG AlaAlaGlnAspAlaValArgAlaSerAlaGlnArgMetGlyAspThrHisThrGlyLeu ATGTTCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTTCGGGAG 1.09e-67 886.00 100.0% 100.0% 84.5% adenocarcinoma, lymphoma, melanoma x AAE03654 (1-185) Length: Matches: Conservative: Gaps: Indels: Mismatches: 185 175 0 0 534 175 160 489 140 429 120 100 80 60 40 129 20 369 309 249

AAB42581 protein;

(first entry

Human ORFX ORF2345 polypeptide sequence SEQ ID NO:4690

ARBSULT 13
AAB42581
ID AAB42
XX AAB42
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XX WHumar
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KW Humar
KW Humar Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; orecopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; osteoarthritis; graft

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifugal; antitheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 3880-3881; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
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05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.:
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ArgGluPheValGlyGlnLeuValAlaProLeuProLeuAlaPro***AlaLeuArgAl
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98.3%
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                                                               New isolated Willebrand Factor A-Related Protein polypeptide useful for
the manufacture of a medicament in the treatment of a disease condition
of the extracellular matrix, in particular arthritis.
                                                                                                               N-PSDB;
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                                            Claim
                                                                                                                                                  Bateman
                                                                                                                                                                                              02-MAY-2001; 2001AU-00004701
                                                                                                                                                                                                                     02-MAY-2002; 2002WO-AU000542
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                                                                                                                                                                                                                                                                                                     Misc-difference
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DB; AAD50400.
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                                           Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; protein; 180
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                                                                                                                                                                                                                                                                                                                                                                       Factor A domain lar matrix; ECM;
                                                                                                                                                Fitzgerald
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                           78-79; 103pp; English
                                                                                                                                                                                                                                                                                                                                                             mouse.
                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .2
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                                                                                                                                                                                                                                                                                                                                                                       related-protein; von Willebrand Factor A; VA; molecular marker; cartilage; arthritis; WARP;
                                                                                                                                                                                                                                                                                                                                                                                                         A (VA) domain.
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The invention relates to Willebrand Factor (WARP) which is a member of von Willebrand superfamily of extracellular matrix (ECM) p

r A domain related-protein d Factor A (VA)-domain prot proteins. WARP is used as

-domain protein
is used as a

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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The
                                                 Willebrand Factor A domain related-protein; von Willebrand Factor A; extracellular matrix; ECM; molecular marker; cartilage; arthritis; W/
                                                                                      Mouse
                                                                                                               24-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 180 AA;
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                                               extracellular
                                    therapy;
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                                                                                     Willebrand
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84.2%
72.6%
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                                                                                     domain related-protein
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Indels:
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Query Match:
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                                                                                                                                                                                                                                                               Alignment
                                                                                                                                                                                                                                                                                                             superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The present sequence is mouse WARP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Willebrand Factor A-Related Protein polypeptide useful the manufacture of a medicament in the treatment of a disease condit of the extracellular matrix, in particular arthritis.
                                                                                                                                                                                                                                                                                       Sequence 415
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                                                                  GTTCGGGAGTTTGTGGGGCAGCTGGTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGT
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                                                  ValargGluPheValGlyGlnLeuValAlaThrMetSerPheGlyProGlyAlaLeuArg
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Search completed: February 13, 2006, 13:23:30 Job time: 97.9481 secs

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Result
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Perfect score:
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-QB-Published Applications AA Main -QPMT-fastan -SUPFIX=rapbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 - MATRIX=blosun62
-TRANS=human40.cdi -LIST=45 -DCCALIGN=20 -THR SCORE-pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=20000000 -HOST=abss02p
-USER=US10699035_0GCN 1 1 405 @runat 13022006_062450_25572 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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                                                                                                                                                                                                                                                                       Score
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seq length: 2000000000
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Match
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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US-10-699-035A-2

US-09-789-561-85

US-09-833-245-2096

US-10-883-936-8

US-09-789-561-165

US-10-883-936-165

US-09-789-561-159

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US-10-699-035A-6

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Sequence 2, Appli
Sequence 85, Appl
Sequence 2096, App
Sequence 85, Appl
Sequence 165, App
Sequence 165, App
Sequence 159, App
Sequence 159, App
Sequence 5, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 18, Appli
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ALIGNMENTS

RESULT 1 US-10-699-035A-2

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APPLICANT: Bateman, John
APPLICANT: Fitzgerald, David
FITTE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838 0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR FILING DATE: 2002-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
                                                          Percent Similarity:
Best Local Similarity:
Query Match:
US-10-699-035A-1 (1-537) x US-10-699-035A-2 (1-180)
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                                                                                                                                  Score:
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                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 40 SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                    LENGTH: 180
TYPE: PRT
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100.0%
100.0%
86.0%
                                                                                                           Length:
Matches:
Conservative:
                                                                 Mismatches:
Indels:
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1 GGGGACCTGATGTTCCTGCTGGACAGCCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCCGG

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CURRENT APPLICATION NUMBER: US/09/789,561
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 85
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                                                                Query Match:
DB:
                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                             NAME/KEY: SITE
LOCATION: (7)
OTHER INFORMATION:
US-09-789-561-85
                                                                                                                              Score:
                                                                                                                                               Pred. No.:
                                                                                                                                                              Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: PZ043P1
                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo
FEATURE:
                                                                                                                                                                                                                                                                                                        ENGTH: 215
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                                      Query Match:
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                                                                                                                                   US-09-833-245-2096
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CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver: 2.1
US-10-699-035A-1 (1-537) x US-09-833-245-2096 (1-215)
                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver.
SEQ ID NO 2096
LENGTH: 215
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NAME/KEY: SITE
LOCATION: (7)
OTHER INFORMATION: )
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ORGANISM: Homo
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Query Match:
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                                                                            Pred. No.:
                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/883,936
CURRENT FILING DATE: 2004-07-06
PRIOR APPLICATION NUMBER: US/09/789,561
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 85, Application US/10883936
Publication No. US20050019866A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: PZ043P1
                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver.
SEQ ID NO 85
LENGTH: 215
                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
                                                                                                                                     LOCATION: (7)
OTHER INFORMATION:
                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                 NAME/KEY: SITE
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APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted prote
FILE REFERENCE: PZ043P1
CURRENT APPLICATION NUMBER: US/09/789,561
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
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US-09-789-561-165
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US-10-699-035A-1 (1-537) x US-09-789-561-165 (1-226)
                                           Query Match:
                                                                                                                                              US-09-789-561-165
                                                                                                    Pred. No.:
                                                                                                                 Alignment Scores:
                                                                                                                                                                                   SOFTWARE: Pac
SOFTWARE: Pac
SEQ ID NO 165
FONGTH: 226
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 165, Application Patent No. US20020064818A1
                                                                                                                                                           LENGTH: 226
TYPE: PRT
ORGANISM: Homo
                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver.
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                                           Length:
Matches:
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US-10-883-936-165
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                                US-10-699-035A-1 (1-537) x US-10-883-936-165 (1-226)
                                                                           Best Local Similarity:
Query Match:
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                                                                                                                                                                                   US-10-883-936-165
                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US/09/789,561
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 165, Application US/10883936
Publication No. US20050019866A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. SEQ ID NO 165
                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: PZ043P1
CURRENT APPLICATION NUMBER: US/10/883,936
CURRENT FILING DATE: 2004-07-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted proteins
                                                                                                                                                                                              LENGTH: 226
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                        No : :
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CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
SEQ ID NO 159
LENGTH: 242
TYPE: PRT
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US-09-789-561-159
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    Percent Similarity:
                 Score:
                                  Pred. No.:
                                             Alignment Scores:
                                                                              US-09-789-561-159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 159, Application US/09789561 Patent No. US20020064818A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: 52 Human secreted proteins FILE REFERENCE: PZ043P1
                                                                                                                                                                                                FEATURE:
NAME/KEY: SITE
LOCATION: (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                   OTHER INFORMATION:
NAME/KEY: SITE
LOCATION: (5)
                                                                                                        NAME/KEY: SITE LOCATION: (34)
                                                                                                                                      OTHER INFORMATION:
                                                                                                                                                                                                                                             ORGANISM: Homo
                                                                                            INFORMATION:
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                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/883,936
CURRENT FILING DATE: 2004-07-06
PRIOR APPLICATION NUMBER: US/09/789,561
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR PPLICATION NUMBER: 60/152,315
PRIOR PILING DATE: 1999-09-03
PRIOR PILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
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                                                                                                                                                          SOFTWARE: Patentin Ver.
SEQ ID NO 159
LENGTH: 242
PEATURE:
NAME/KEY: SITE
                                                        ORGANISM: Homo sapic
FEATURE:
FEATURE:
NAME/KEY: SITE
LOCATION: (2)
OTHER INFORMATION: )
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                                                                                                                                              TYPE: PRT
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APPLICANT: Bateman, John
APPLICANT: Pitzgerald, David
ITITLE OF INVENTION: A Molecular Marker
ITITLE OF INVENTION: A Molecular Marker
ITITLE OF INVENTION: A MOLECULAR A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 418
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                                                                                                                                                                                                                  Sequence 6, Application US/10699035A Publication No. US20040214349A1 GENERAL INFORMATION:
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NAME/KEY: SITE
LOCATION: (34)
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APPLICANT: Bateman, John
APPLICANT: Fitzgerald, David
APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-010-31
PRIOR APPLICATION NUMBER: PC7
PRIOR APPLICATION NUMBER: PC7
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR PILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEG ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
                                                                                                                                                                                               RESULT 10

US-10-699-035A-20

; Sequence 20, Application US/10699035A

; Publication No. US20040214349A1

; GENERAL INFORMATION:
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Query Match:
DB:
Alignment
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                     US-10-699-035A-20
                              TYPE: PRT ORGANISM: Homo sapiens
                                                  LENGTH: 418
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Percent Similarity:
Best Local Similarity:
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US-10-149-819-18
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DB:
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APPLICANT: YUE, Henry
APPLICANT: AZMEAI, Yalda
APPLICANT: TANG, Y. Tom
APPLICANT: BATTERSON, Chand
APPLICANT: BAUGHN, Mariah R
APPLICANT: LU, Dyung Aina M
                                             CURRENT APPLICATION NUMBER: US/10/149,819
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/172,852; 60/172,354
PRIOR FILING DATE: 1999-12-10; 1999-12-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL Program
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/10149819
Publication No. US20030044913A1
                                                                                                                                                                 APPLICANT: LU, Dyung Aina M.
APPLICANT: SHAH, Purvi
APPLICANT: LAL, Preeti
APPLICANT: BURYOUNG, Janice
APPLICANT: BURYORD, Neil
TITLE OF INCENTION: EXTRACELLULAR MATRIX AND
FILE REFERENCE: PF-0760 PCT
TYPE: PRT
ORGANISM: Homo
                               LENGTH: 185
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APPLICANT: Bateman, John
APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PAID PRIOR PILING DATE: 2002-05-02
PRIOR PILING DATE: 2002-05-02
PRIOR PILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 8
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Best Local Similarity:
Query Match:
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US-10-699-035A-8
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID
US-10-149-819-18
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                                                                                                                                                                                                                                                     Sequence 8, Application US/10699035A Publication No. US20040214349A1 GENERAL INFORMATION:
10-699-035A-8
            LENGTH: 180
TYPE: PRT
ORGANISM: Mus musculus
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APPLICANT: DACEMAN; David
APPLICANT: BITGGETAID, David
APPLICANT: HITGGETAID, David
FILE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR PILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 31
LENGTH: 181
                                                                                                                                                                                                                          RESULT 13
US-10-699-035A-31
Sequence 31, Application US/10699035A
Publication No. US20040214349A1
GENERAL INFORMATION:
APPLICANT: Bateman, John
APPLICANT: Fitzgerald, David
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Alignment

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Best
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TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
FURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
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US-10-699-035A-4
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Best Local Similarity:
                Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10699035A Publication No. US20040214349A1
                                                                                                SEQ ID NO 4
LENGTH: 415
TYPE: PRT
ORGANISM: Mus musculus
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                                                                                                                                                        APPLICANT: FITZGETAID, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PC7/AU02/00542
PRIOR FILING DATE: 2002-05-02
PRIOR PPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SOPTWARR: FASTSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 415
TYPE: PRT
ORGANISM: Mus musculus
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   US-10-699-035A-1 (1-537)
                                                                                                         Pred. No.:
                                                                                                                      Alignment Scores:
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Search completed: February 13, 2006, 13:53:23 Job time: 91.701 secs

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US-08-897-443-1

US-09-907-794A-34

US-09-905-125A-34

US-09-902-775A-34

US-09-903-603A-34

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ALIGNMENTS

RESULT 1 US-09-513-999C-6277

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.

Sequence 6277, Application US/09513999C Patent No. 6783961

Query Match: DB: Percent Similarity: Best Local Similarity: Pred. No.: US-10-699-035A-1 (1-537) x US-09-513-999C-6277 (1-77) Alignment Scores: ; OTHER INFORMATION: US-09-513-999C-6277 NUMBER OF SEQ ID NOS: 36681 SOFTWARE: Patent.pm SEQ ID NO 6277 LENGTH: 77 TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins Patent No. 6783961CURRENT APPLICATION NUMBER: US/09/513,999C CURRENT FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26 FILE REFERENCE: 59.US2.REG LENGTH: 77
TYPE: PRT
ORGANISM: Homo sapiens FEATURE: NAME/KEY: UNSURE LOCATION: 66 2.51e-26 384.00 98.7% 98.7% 36.6% 2 Xaa=Cys or Gly Conservative: Mismatches: Indels: Length: Matches: 77 0 1 0

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Query Match:
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; ORGANISM: Human
US-09-949-016-10340
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION DATE: 2000-09
NUMBER OF SEO ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-949-016-10340
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307
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PRIOR FILING DATE: 2000-10-20
PRIOR PPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION.
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Patent No. 6812339
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CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
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                                                                                   CCCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGA 420
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Patent No. 5981263
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IMMEDIATE SOURCE:
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FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                      LIBRARY: U.L. CNE: 681719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM CON
OPERATING SYSTEM:
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                                                        CGGGAGTTTGTGGGGCAGCTGGTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGTGCC
                                                                                 : 638 amino acids amino acid
 AGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCCTTCGGCCAGCACAGCTCG
                             LysGluPheIleValAspIleLeuGlnPheLeuAspIleGlyProAspValThrArgVal 96
                                                                                                              GACCIGATGITCCTGCTGGACAGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTT
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Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                              415-845-4166
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APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: DS 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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                       APPLICATION NUMBER: PCT/US99/20594 FILING DATE: 1999-09-08
  APPLICATION
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Gao, Wei-Qiang
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Grimaldi, Christopher J.
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Gerritsen, Mary E.
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Timothy A.
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
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APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: PCT/US99/30999
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CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: DCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PILING DATE: 1999-10-05
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                     FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US99/30999
FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US00/00219
FILING DATE: 2000-01-05
                                                                                                                                FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
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APPLICATION NUMBER: PCT/US99/28564
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Williams, P. Mickey
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Hillan, Kenneth, J.
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Botstein, David
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art, Timothy A.
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ff, Ellen
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LENGTH: 915
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                                                                                                                                                                                                                                                                                                                      Patent No. 668645
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Gao, Wei-Qiang
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Godowski, Paul J.
Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth, J.
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                                                                                           Gerber, Hanspeter
Gerritsen, Mary E
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT FILING DATE: 2001-07-10
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APPLICATION NUMBER: US 60/143,048
FILING DATE: 1999-07-07
APPLICATION NUMBER: US 60/145,698
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FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
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APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
FILING DATE: 1999-10-05
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FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
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APPLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-08
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APPLICATION NUMBER: US 60/146,222
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                      LysGluPheIleValAspIleLeuGlnPheLeuAspIleGlyProAspValThrArgVal
                                                                                       Roy, Margaret
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CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-07-28
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
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Grimaldi, Christopher J.
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Gao, Wei-Qiang
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Ashkenazi, Avi
Botstein, David
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Eaton, Dan L.
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CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
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PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
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APPLICATION NUMBER: PCT/US99/28564
FILING DATE: 1999-12-02
                                  APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US99/30999
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FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
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Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
' vliavin, Ivar J.
' vliavin, Ivar J.
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Gerritsen, Mary E.
Goddard, A.
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Botstein, David
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Mather, Jennie P.
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Filvaroff, Ellen
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art, Timothy A.
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SEQ ID NO 34
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                                                                                                                                                                                                                        Sequence 34, Application Patent No. 6806352
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APPLICANT: Ashkenazi
APPLICANT: Botstein,
APPLICANT:
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                                                    Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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             Godowski,
Grimaldi,
                                                                                                             Ferrara, Napoleone
Filvaroff, Ellen
Gurney,
                                          Goddard,
                                                                                                                                        Desnoyers, Luc
Eaton, Dan L.
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PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/2059
PRIOR FILING DATE: 1999-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14 CURRENT APPLICATION NUMBER: US/09/904,920A CURRENT FILING DATE: 2001-07-13 PRIOR APPLICATION NUMBER: PCT/US00/04414 PRIOR PILING DATE: 2000-02-22 PRIOR PILING DATE: 2000-02-22 PRIOR APPLICATION NUMBER: US 60/143,048 PRIOR FILING DATE: 1099-07-07 PRIOR APPLICATION NUMBER: US 60/145,698 PRIOR APPLICATION NUMBER: US 60/145,698
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PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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PRIOR APPLICATION NUMBER: PCT/US99/28565
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APPLICATION NUMBER: PCT/US99/30095
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LysGluPheIleValAspIleLeuGlnPheLeuAspIleGlyProAspValThrArgVal
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Kljavin, Ivar J.
Mather, Jennie P
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Patent No. 6818449
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                                                                   CURRENT APPLICATION NUMBER: US/09/909,064
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
                                                                                                                                                                                                                 APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                   FILING DATE: 1999-07-26
APPLICATION NUMBER: US 60/146,222
FILING DATE: 1999-07-28
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Botsteir
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Gao, Wei-Qiang
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Stewart, Timothy A.
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Gerritsen, Mary E.
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Filvaroff, Ellen
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Eaton, Dan L.
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NUMBER: PCT/US99/20594
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APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US99/30999
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APPLICATION NUMBER: PCT/US99/20944
FILING DATE: 1999-09-13
LAPPLICATION NUMBER: PCT/US99/21090
R FILING DATE: 1999-09-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US99/21547
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FILING DATE: 1999-12-02
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                                    GGCCGAGGCAACTTCCTGGAGCTGTCAGCCGCTGAGCCCCTGCCGAGAAGCACCTG 474
                                                                                                                                                 LeuArgGluAsnValProArgValIleMetIleValThrAspGlyArgProGlnAspSer
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 GlyGlnValAspPheAsnThrLeuLysSerIleGlySerGluProHisGluAspHisVal
                                                                         ValAlaGluValAlaAlaLysAlaArgAspThrGlyIleLeuIlePheAlaIleGlyVal 196
                                                                                                            GTGGGCCCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACC
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                                                 CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: DCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PRIOR PAPPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/2054
PRIOR APPLICATION NUMBER: PCT/US99/2094
PRIOR PILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
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PRIOR APPLICATION NUMBER: PCT/US99/300911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CUBERSNM ROWS.
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APPLICANT: Ashkenazi, Avi
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    FILING DATE:
APPLICATION I
                                         APPLICATION NUMBER: PCT/US99/30999
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Mather, Jennie P.
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Grimaldi, Christopher
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Gerritsen, Mary E.
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Filvaroff, Ellen
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Eaton, Dan L.
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Botstein, David
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art, Timothy A.
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; ORGANISM: Homo 8
US-09-905-381A-34
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NUMBER OF SEQ ID NOS: 423
SEQ ID NO 34
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Patent No. 6828146
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                                                                                                                                                                                              : Genentech, Inc.
: Ashkenazi, Avi
: Botstein, David
: Desnoyers, Luc
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                                                                                  Fong, Suc....
Gao, Wei-Qiang
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Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
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                                                         Gerritsen, Mary
                                                                               Gerber, Hanspeter
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Filvaroff, Ellen
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Best Local Similarity:
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US-09-906-618-34
                                                                                                                                                                                             Pred. No.:
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LENGTH: 915
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ORGANISM:
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NUMBER OF SEQ ID NO
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PRIOR FILING DATE: 2000-02-22
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CURRENT FILING DATE: 2001-07-16
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
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APPLICATION NUMBER: PCT/US99/20944
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APPLICATION NUMBER: PCT/US99/23089
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APPLICATION NUMBER:
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APPLICATION NUMBER: PCT/US99/30911
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Mather, Jennie P.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,646
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
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Roy, Margaret Ann
Stewart, Timothy A.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher
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Eaton, Dan L.
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IOR APPLICATION NUMBER: PCT/US99/30911
IOR APPLICATION NUMBER: PCT/US99/30999
IOR APPLICATION NUMBER: PCT/US99/30999
IOR APPLICATION NUMBER: PCT/US99/30999
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IOR APPLICATION NUMBER: PCT/US00/00219
IOR FILING DATE: 2000-01-05
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FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
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FILING DATE: 1999-11-29
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APPLICATION NUMBER: PCT/US99/21090
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FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
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GGCCGAGGCAACTTCCTGGAGCTGTCAGCCGCTGAGCCCCTGCCGAGAAGCACCTG
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Db 197 GlyGlnValAspPheAsnThrLeuLysSerIleGlySerGluProHisGluAspHisVal 216
Qy 475 ------CACTTTGTGGACGTGGACGTGACATCATTGTCCAAGAG 516
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Search completed: February 13, 2006, 13:43:34 Job time: 25.7889 secs

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PheLeuValAlaAsnPheSerGlnIleGluThrLeuThrSerValPheGlnLys 234

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-DB=PIR -QFMT=fastan -SUFFIX=Typ -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=DIOSUM62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN-0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss02p
-USER=US10699035_0CGN 1 1 77 @FUNBAL 13022006_062444_25463 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBI-OCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XCAPOP=10 -XCAPEXT=0.5 -FGAFOP=6 -FGAFEXT=7
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A;Accession: A2803/ A;Molecule type: mRNA A;Residues: 2960-2976,'P',2978-3074,'AG' <gor3> A;Essidues: 2960-2976,'P',2978-3074,'AG' <gor3> A;Cross-references: UNIPARC:UPI00001712P4; EMBL:M17375; NID:g211649; PIDN:AAA48718.1; P A;Note: this sequence has been revised in reference A34485</gor3></gor3>	A;Reference 1702-2792;2446-2873 <gor2> A;Cross-references: UNIPARC:UPI0000173C40 A;Cross-references: UNIPARC:UPI0000173C40 A;Cross-references: UNIPARC:UPI0000173C40 A;Cross-references: UNIPARC:UPI0000173C40 A;Cordon, M.K.; Gerecke, D.R.; Olsen, B.R. Proc. Natl. Acad. Sci. U.S.R. 84, 6040-6044, 1987 A;Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA A;Reference number: A28037; MUID:87317590; PMID:3476925</gor2>	A; No George Control A; No George Control A; No George Control A; Residues: 2456-2758; A; 2760-2802; F; 2804-2976; F; 2978-3124 <gor> A; Residues: 2456-2758; A; 2760-2802; F; 2804-2976; F; 2978-3124 <gor> A; Cross-references: UNIPARC: UPI0000171233; EMBL: J05137; NID: G211284; PIDN: AAAA48635.1; P A; Accession: B34485 A; Accession: B34485</gor></gor>	A;Residues: 1-3124 <yam> A;Residues: 1-3124 <yam> A;Cross-references: UNIPROT:P13944; UNIPARC:UPI0000126D2D; GB:D00824; NID:g222810; PIDN A;Cross-references: UNIPROT:P13944; UNIPARC:UPI0000126D2D; GB:D00824; NID:g222810; PIDN A;Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and, R;Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R. J. Biol. Chem. 264, 19772-19778, 1989 J. Biol. Chem. 264, 19772-19778, 1989 A;Title: Type XII collagen. A large multidomain molecule with partial homology to type A;Feference number: A34485; MUID:90062079; PMID:2584192 A.Accession. A34485</yam></yam>	C;Species: Gallus galius (Chicken) C;Species: Gallus galius (Chicken) C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004 C;Accession: A40020; A34485; B34485; A28037; S23814; S22254; S28811 R;Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Oba J. Cell Biol. 115, 209-221, 1991 A;Title: The complete primary structure of type XII collagen shows a chimeric molecule nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site A;Reference number: A40020; MUID:92011862; PMID:1918137 A;Accession: A40020 A;Molecule type: mRNA	RESULT 1 A40020 Collagen alpha 1(XII) chain precursor - chicken N;Alternate names: fibrochimerin

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C; Generics:

A; Introns: 2845/3; 2863/3; 2887/3; 2899/3; 2922/1; 2985/1; 3008/1; 3065/1 C; Keywords: alternative splicing; cell binding; coiled coil; connective tissue F; 24-3124/Product: collagen alpha 1(XII) chain short splice form #status F; 24-3114/Domain: IIIA #status predicted <XIG>
F; 24-3124/Product: collagen alpha 1(XII) chain short splice form #status F; 24-114/Domain: IIIA #status predicted <XIIIA>
F; 24-114/Domain: IIIB #status predicted <XIIIA>
F; 24-105/Domain: fibronectin type III repeat homology <FW3A>
F; 332-425/Domain: fibronectin type III repeat homology <FW3A>
F; 332-414/Domain: fibronectin type III repeat homology <FW3C>
F; 320-1718/Domain: fibronectin type III repeat homology <FW3C>
F; 320-1718/Domain: fibronectin type III repeat homology <FW3C>
F; 321-802/Domain: fibronectin type III repeat homology <FW3C>
F; 321-404/Domain: fibronectin type III repeat homology <FW3C>
F; 321-404/Domain: fibronectin type III repeat homology <FW3C>
F; 324-405/Domain: fibronectin type III repeat homology <FW3C>
F; 334-4165/Domain: fibronectin type III repeat homology <FW3C>
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A;Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517,'A;Residues: 'X',1333,'Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517,'A;Rossidues: 'X',1335,'Q',1355-1347;10000173C42; UNIPARC:UPI0000173C43, R;Dublet, B.; van der Rest, M.
R;Dublet, B.; van der Rest, M.
J. Biol. Chem. 262, 17724-17727, 1987
A;Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of pepsin-A;Reference number: S22254; MUID:88087065; PMID:3121603
A;Accession: S22254
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Eur. J. Biochem. 207, 847-856, 1992
A;Title: A major oligomeric fibroblast proteoglycan identified
A;Reference number: S23814; MUID:92362621; PMID:1323460
A;Accession: S23814
  Best Local Similarity:
Query Match:
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A;Residues: 1-24,1189-1257,'S',1259-1263,'E',1265-1280
A;Cross-references: UNIPARC:UPI0000173C46; EMBL:X67327
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A;Title: The two splice variants of collagen XII share a
A;Reference number: S28811; MUID:93042014; PMID:1420368
A;Accession: S28811
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A;Residues: 2831-2832,'T',2834,'R',2836-2843;3002-3014 <DUB>
A;Cross-references: UNIPARC:UPI0000173C44; UNIPARC:UPI0000173C45
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                                                    AlaProGlyAsn-----ValLeuArgTyrArgLeuValTyrArgProLeuThrGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgProAsnValProArgValMetIleLeuIleThrAspGlyLysSerSerAspAlaPhe
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A; Notecule type: mUNA
A; Residues: 815-892, 'E', 894-1439 <PAR>
A; Residues: 815-892, 'E', 894-1439 <PAR>
A; Cross references: UNIPARC: UDIO0016A722; GB:M65158; GB:S49017; NID:g180914; PIDN:AAA96
A; Experimental source: keratinocyte
R; Gammon, W.R.; Abernethy, M.L.; Padilla, K.M.; Prisayanh, P.S.; Cook, M.E.; Wright, J.;
J. Invest. Dermatol. 99, 691-696, 1992
A; Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion prot
A; Reference number: 156328; MUID:93107742; PMID:1469284
A; A; Recession: 156328
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 'EFR', 372-517, 'DV', 520-540, 'W', 542-1255 <RES>
A; Cross-references: UNIPARC: UDI00016B3AC; GB:S51236; NID:g262308; PIDN:AAB24637.1; PID:
A; Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgeson, R.E.
A; Title: Cleavage of type VII collagen by interstitial collagenase and type IV collagena
A; Reference number: A30296; MUID:89139437; PMID:2537292
A; Accession: A30296
A; Molecule type: protein.
A; Molecule type: UNIPARC: UNIPARC: UPI000017A13B; UNIPARC: UPI000017A13C;
A; Note: two reported peptides cannot be reliably located
R; Greenspan, D.S.
Hum. Mol. Genet. 2. 273-278. 1993

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A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: the authors translated the codon ACC for residues 394 and 397 as Tyr R;Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A;Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the QA;Reference number: S16316; MUID:91334380; PMID:1871109
A;Accession: S16316
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C;Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_chang
C;Date: 04-Nov-1994 #sequence_revision 04-Nov-1996; I84686
C;Accession: A54849; PH0844; S16316; I56328; A30296; I84686
R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J.
J. Biol. Chem. 269, 20256-20262, 1994
A;Title: Cloning of human type VII collagen. Complete primary
A;Reference number: A54849; MUID:94327588; PMID:8051117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-2944 <CHR>
A;Residues: 1-2944 <CHR>
A;Cross-references: UNIFROT:Q02388; UNIPARC:UPI000017A138; GB:L02870; NID:g987124; PIDN R;Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S.
B;Cranaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S.
Biochem. Biophys. Res. Commun. 183, 958-963, 1992
                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 2395-2871, S', 2873-2944 KBE2>
                                                                                                                                                        Hum. Mol. Genet. 2, 273-278, 1993
A; Title: The carboxyl-terminal half of type
A; Reference number: 148103; MUID:93271985; I
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A;Residues: 'EFR',340-475,'RALSTASHSTLCWRATRWHDCNRGSHWTRAACEDCNRDASHRAARAG',524-528,'C'
A;Cross-references: UNIPARC:UPI000017A139; DDBJ:D11152; DDBJ:D13694; NID:g453698; PIDN:
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A;Status: not compan
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N;Alternate names: procollagen alpha 1(VII) chain
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Cross-references: UNIPARC:UPI000016A724; GB:L06862; NID:g388713; PIDN:AAA89196.1;
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Best Local Similarity:
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A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.:
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F;1052-1219/Domain: von Willebrand factor type A repeat homology <PWA2>
F;1170-1172/Region: cell attachment (R-G-D) motif
F;1189-1253/Region: cysteine/proline-rich
F;1254-2783/Region: interrupted helical
F;1254-2783/Region: cell attachment (R-G-D) motif
F;1334-1336/Region: cell attachment (R-G-D) motif
F;108-2010/Region: cell attachment (R-G-D) motif
F;208-2010/Region: cell attachment (R-G-D) motif
F;2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
F;2784-2944/Domain: animal Kunitz-type proteinase inhibitor homology <API>F;2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <API>F;2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <API>F;2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <API\F;28753-2553-251/Modified site: 5-hydroxylysine (Lys) #status experimental
F;2625,2631/Modified site: 5-hydroxylysine (Lys) #status experimental
F;2625,2631/Binding site: carbohydrate (Lys) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;231-318/Domain: fibronectin type III repeat homology FN15
F;327-413/Domain: fibronectin type III repeat homology FN27
F;414-502/Domain: fibronectin type III repeat homology FN3
F;408-93/Domain: fibronectin type III repeat homology FN3
F;508-93/Domain: fibronectin type III repeat homology FN5
F;598-683/Domain: fibronectin type III repeat homology FN5
F;686-71/Domain: fibronectin type III repeat homology FN7
F;706-862/Domain: fibronectin type III repeat homology FN8
F;954-1045/Domain: fibronectin type III repeat homology FN8
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Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994

A;Title: Dominant dystrophic epidermolysis bullosa: identification of a A;Reference number: A55255; MUID:94224777; PMID:8170945

A;Contents: annotation
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A;Note: defects in this gene can result in dominant and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Comment: Prolines and lysines at the third position of ed and subsequently O-glycosylated.
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                                                                                                                                                                                                                                        217 GCCAGTCTGGTGCACGTGGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGC
                                                                                                                                  163 GAGTTTGTGGGGCAGCTGGTGGCTCCACTGCCCCTGGGCACCGGGGCC-----CTGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetThrLeuArgLeuLeuValAlaAlaLeuCysAla-----GlyIleLeuAlaGluAla
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                                                                                                         SerGlnAspAspValIleProProAlaLysAsnLeuArgAspAlaGlyIleGluLeuPhe
                                                                                                                                     TCCAGCGACCCTGTGGGCCCCCCCATGCAGGACCTCAAGGACCTGGGCGTCACCGTGTTC
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609 310 498 270 438 250 378 230 318

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C;Reywords: alternative splicing; coiled coil; extracellular matrix; F:1-28/Domain: signal sequence #status predicted <SIG>F:1-28/Domain: signal sequence #status predicted <SIG>F:29-1857/product: collagen alpha 1(XIV) chain, short form #status p F:29-110/Domain: fibronectin type III repeat homology <FN3A>F:156-320/Domain: fibronectin type III repeat homology <FN3B>F:352-433/Domain: fibronectin type III repeat homology <FN3B>F:442-525/Domain: fibronectin type III repeat homology <FN3C>F:534-614/Domain: fibronectin type III repeat homology <FN3B>F:623-707/Domain: fibronectin type III repeat homology <FN3F>F:741-823/Domain: fibronectin type III repeat homology <FN3F>F:741-823/Domain: fibronectin type III repeat homology <FN3F>F:832-914/Domain: fibronectin type III repeat homology <FN3F>F:832-914/Domain: fibronectin type III repeat homology <FN3B>F:922-1009/Domain: fibronectin type III repeat homology <FN3H>F:1040-1205/Domain: fibronectin type III repeat homology <
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C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003
C;Accession: S31212
R;Waelchli, C:; Trueb, J:; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Bur. J. Biochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: S31211; MUID:93185668; PMID:8444186
A;Accession: S31212
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A; Residues: 1-1857 <WAE>
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Best Local Similarity:
ProAlaIleAla-----AspIleValIleLeuValAspGlySerTrpSerIleGly
                                                                                                                  1.1e-14
382.00
43.8%
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           170
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submitted to the EMBL Data Library, January 1993

A; Reference number: S78476

A; Reference number: S78476

A; Accession: S78476

A; Molecule type: mRNA

A; Cross-references: UNIPATC: UNIPARC: UPI0000126D31;

A; Cross-references: UNIPATC: B:; Winterhalter, K.H.;

R; Waelchli, C:, Trueb, J:; Kessler, B:; Winterhalter, K.H.;

Eur. J. Biochem. 212, 483-490, 1993

A; Title: Complete primary structure of chicken collagen XIV

A; Reference number: S31211; MUID:93185668; PMID:8444186

A; Accession: S31211

A; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-416;1460-1811,1843-1888 <WAE>

A; Cross-references: UNIPARC: UPI00001773F4; UNIPARC: UPI00001

C; Genetics:
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578476
collagen alpha 1(XIV) chain precursor,
collagen sellus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision
C;Accession: S78476; S31211
R;Trueb, B.
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   ;Status: preliminary
;Molecule type: mRNA
;Residues: 1-416;1460-1811,1843-1888 <WAE>
;Cross-references: UNIPARC:UPI00001773F4; UNIPARC:UPI00001773F5; EMBL:X70793
;Genetics:
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                     ValSerTrp-
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A;Gene: Col14A1

C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein;

F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1888/Product: collagen alpha 1(XIV) chain, long form #status predicted <MAT>
F;29-110/Domain: fibronectin type III repeat homology <FN3A>
F;156-320/Domain: fibronectin type III repeat homology <FN3C>
F;352-433/Domain: fibronectin type III repeat homology <FN3C>
F;352-433/Domain: fibronectin type III repeat homology <FN3D>
F;442-525/Domain: fibronectin type III repeat homology <FN3D>
F;533-614/Domain: fibronectin type III repeat homology <FN3B>
F;623-707/Domain: fibronectin type III repeat homology <FN3B>
F;741-823/Domain: fibronectin type III repeat homology <FN3F>
F;832-914/Domain: fibronectin type III repeat homology <FN3F>
F;832-914/Domain: fibronectin type III repeat homology <FN3G>
F;922-1009/Domain: fibronectin type III repeat homology <FN3G>
F;932-1009/Domain: fibronectin type III repeat homology <FN3G-
F;932-1009/Domain: fibronectin type III repeat homology
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ThrHisSerProGlyLysValGluLysTyrArgValVal

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A45974

collagen alpha 1(XIV) chain precursor, short form 2 - chicken

N,Alternate names: unduin

C;Species: Gallus gallus (chicken)

C;Species: I0-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004

C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004

C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: A45974; S30085; S22916; S17035; S20833

R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Canc

J. Biol. Chem. 268, 12177-12184, 1993
A;Molecule type: mRNĀ
A;Restdues: 286-494,'Q',496-834,'A',836-1119,'KL',1122-1402,1409-1439
A;Cross-references: UNIPARC:UPI0000173C48
R;Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der
                                                                                                  A;Cross-references: UNIPARC:UPI00000006A2; EMBL:X65122; NID:g62871; R;Trueb, J.; Trueb, B.
Eur. J. Biochem. 2007, 549-557, 1992
A;Title: Type XIV collagen is a variant of undulin.
A;Reference number: S22916; MUID:92339443; PMID:1339349
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                                                                    A;Accession: S22916
A;Status: preliminary
                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1472-1660 <APT>
                                                                                                                                                                                                                          A; Reference number: A; Accession: S30085
                                                                                                                                                                                                                                          submitted to the EMBL Data A; Reference number: S30085
                                                                                                                                                                                                                                                                                                               A; Experimental source: embryo skin A; Note: sequence inconsistent with the nucleotide translation
                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: mRNA; protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A45974; MUID: 93280195; PMID: 8505337
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A; Residues: 1472-1659
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F;40-204/Domain: von Willebrand factor type A repeat homology <N3A>F;236-401/Domain: fibronectin type III repeat homology <N3A>F;326-409/Domain: fibronectin type III repeat homology <PN3B>F;418-498/Domain: fibronectin type III repeat homology <PN3C>F;507-591/Domain: fibronectin type III repeat homology <PN3C>F;507-591/Domain: fibronectin type III repeat homology <PN3D>F;625-707/Domain: fibronectin type III repeat homology <PN3E>F;716-798/Domain: fibronectin type III repeat homology <PN3G>F;806-893/Domain: fibronectin type III repeat homology <PN3G>F;806-893/Domain: von Willebrand factor type A repeat homology <FN3G>F;924-1089/Domain: non-collagenous NC4 #status predicted <NC4>F;1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>F;1554-1659/Domain: triple helical domain COL1 #status predicted <NC2>
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A; Residues: 1551-1570; 1593-1599; 1639-1667 < GOR2>
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A;Title: Cloning of a cDNA for a new member of the class of fibril-associated
A;Reference number: S17035; MUID:92037585; PMID:1935930
A;Accession: S17035
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SerThrHisValTyrAsnValAlaAspPheAsnPheMetAsnSerIleValGluGlyLeu
                                                            GAGAAGCACCTGCACTTTGTG---GACGTGGATGACCTGCACATCATTGTCCAA-----
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R;Wei, Y.; Yang, E.V.; Klatt, K.P.; Tassava, R.A.

Dev. Biol. 168, 503-513, 1995

A;Title: Monoclonal antibody MT2 identifies the urodele alp
A;Reference number: I51027; MUID:95246925; PMID:7729585

A;Accession: I51027

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-929 <WEI>
A;Cross-references: UNIPROT:091145; UNIPARC:UPI0000126D2E;
F;155-236/Domain: fibronectin type III repeat homology <3FR
F;631-795/Domain: von Willebrand factor type A repeat homol
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                             GlyThrGlnThrThrThrValLeuValGlyLeuLysProGluThrGluTyrTyrValAsn
                                                                                   GCGGGCCGCAACTGCACGCTGCAGGGCCTGGCGCCGGCCACCGCCTACCTGGTGACC
                                                                                                                                      argPheLysValGluTyrTyrProValAlaGlyGlyArgProGlnGluValTyrValArg
                                                                                                                                                                                                  GGCTACCACGTGCAGTTCGGGCCGCTGCGGGGCGGGGGAGGCGCAGCGGGTGGAGGTGCCC
                                                                                                                                                                                                                                                        ProThrProArgSerPheArgValThrTrpValProPro-----SerGlnSerValGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaArgLysIleAlaIleLeuLeuThrAspGlyLysSerGlnAspAspIleValAlaPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGGCTGCCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCACACTGGC 342
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A; Molecule type: mRNA
A; Residues: 1-843 < JUS>
A; Cross-references: UNIPROT: Q05707; UNIPARC: UPI00000716A9; GB: M64108; NID: g340081;
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DB:
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A;Title: Undulin is a novel member of the fibronectin-tenascin family of extracellular A;Reference number: A40970; MUID:91373351; PMID:1716629
A;Accession: A40970
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J. Biol. Chem. 266, 17326-17332, 1991
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: A40970
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                                  HisAlaIleThrGlyProProThrGluLeuIleThrSerGluValThrAlaArgSerPhe
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                                                                                                                                                                                                                                                                                                                                                           A,Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome. A,Reference number: A03794; MUID:84270667; PMID:6087149
A,Reference number: A03794; MUID:84270667; PMID:6087149
A,Contents: annotation; protein coding region
C,Comment: The sequence contains four perfect repeats (residues 149-273, 274-398, C,Superfamily: human herpesvirus 4 BHLF1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P03181; UNIPARC:UP1000000CC0
R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.;
Nature 310, 207-211, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, E Mol. Biol. Med. 1, 21-45, 1983
A;Tille: Sequence analysis of the 17,166 bp EcoRI fragment A;Reference number: A93065; MUID:85035713; PMID:6092825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BHLF1 protein - human herpesvirus 4 (strain B95-8) C;Species: human herpesvirus 4, Epstein-Barr virus C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 C;Accession: A03742
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A; Residues: 1-660 <BAN>
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Best Local Similarity:
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                                                              US-10-699-035A-5 (1-1254) x QQBE3
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         GGCGCTCGGCCTGGGCCTGAGCTTGCGGCTGGCGCTGGCGCGGAGCGGCGGAGCGCGG
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Conservative:
Mismatches:
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Alignment Scores: 5.42e-07	777 GCTGCCAGGGAACGCCACGGACTGGATCTGGGCCGGCCTCGACCCGGACACGGACTACGA 836
F;37-264/Domain: von Willebrand fan F;225-260/Domain: EGF homology <egf;270-434 domain:="" f.<="" th="" von="" willebrand=""><th>747CGCCCAGCCGGG</th></egf;270-434>	747CGCCCAGCCGGG
A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 78-493 <arg> A;Cross-references: UNIPARC:UPI000 C:Suberfamily: catrilage matrix nr</arg>	699 CCTGCTGACCGCAGACTCCGGGCTACTATGTGCTGGAGCTGGTGCCCAG 746
Acad. Sci. U.S.F. ructural features number: A26364;	654 TGCCACGGAGATCACGTCCAGCGGCTTCCGCCTGGCCTG
A; Molecule type: DNA A; Residues: 1-493 < KIS> A; Cross-references: UNIPROT: P05099 R. Argraves W. S. Deak F. Sparks	597CATCATTGTCCAAGAGCTGAGGGGCTCCATTCTCGCGATGCGGCCGCAGCAGCAGCTCCA 653
A;Reference number: A33809; MUID:8 A;Accession: A33809; MUID:8 A;Status: preliminary	Ala
R;Kiss, I.; Deak, F.; Holloway Jr. J. Biol. Chem. 264, 8126-8134, 198 A;Title: Structure of the gene for	
A33809 cartilage matrix protein precursor C;Species: Gallus gallus (chicken) C;Date: 09-Mar-1990 #sequence_revi C;Accession: A33809: A26364	483 GGG
Db 603 rg 603	
1251	242 LeuAlaAlaAlaGlnArgCysProAlaGlyProProProThrArgSerGlyAla 259 423 GGTGACAGATGGCGGCTCCAGCGACCCTGTGGGGCCCCCCCATGCAGGAGCTCAAGGACCT 482
Qy 1211TGCCCGCGCGCCC Db 583 erGlyAlaThrProHisPro	366 ACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCCAGGGGTGCCCAAAGTGCTGGTGTG 422
Db 563 laProGlyAlaProGlyThr	339 TGGCCTGGCGCTGGT
Db 543 lyHisProProProGlyAla Qy 1152 GAGCGCGCTGTCCGCCAAGG	
1122	185 ArgProAlaAlaProGlyAlaProGlyThrProAlaAlaProGlyProGly 201 297 TGCGGTGCGTGCTTC
Qy 1065 GGGCCGCAACTGCACCACGC :::	CAGTCGGCCATACACCGAGTTCCCCCTTCGGCCAGCACAGCTCGGGTGAGGCTGCCCAGGA
roPro	228 GCACGTGGG 236 ::: AlaGlnArgGlyHisProProProGlyAlaGlyGlnArgProSerGlyProThrGlyGly 184
Db 484GlnGluProArgLeuPro	145 GlnValGlnTrpSerAlaArgAsnProGlyCysProArgThrTrpArgArgArgSerGly 164
Db 464 roGluArgGlySerGlyPro Qy 984 GGGCTCAGÇÇÇÇGGGCGCTCG	COMPTICTICCHOGGIFTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
445 945	GTTCTGCTGGACAGCTCAGCCAGCGTCTCTCACTA
	75 TCCACCAGCATCAGCCCCCCGAGGGGACCTGAT 107 :::
Db 408 ThrTrpArgArgArgSerGl Oy 837 CGTGGCGCTAGTGCCTGAGT	 65 GlyAlaArgProGlyGlyAsnArgValGlyAlaGlyArgGlyArgProGlyThrPro 84

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00004F1EE; GB:M14792; NID:G211545; PIDN:AAA48695.1; PID protein; EGF homology; von Willebrand factor type A repeat homology <VWA1>
EGF>
factor type A repeat homology <VWA2>
                                                                                                                                                                                                                                         99; UNIPARC:UPI000004F1EF; GB:X12346; GB:X12347; GB:X12
ks, K.J.; Kiss, I.; Goetinck, P.F.
, 464-468, 1987
cartilage matrix protein deduced from cDNA.
:87092429; PMID:3025875
                                                                                                                                                                                                                                                                                                                                                                                                                                                or cartilage matrix protein, a modular protein of the enplement factors B and C2, and epidermal growth factor:89255246; PMID:2542265
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OGlnAspLeuAlaAlaAlaGlnArgCysProAlaGlyProP 503
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    chicken

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Length:
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  493
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US-10-699-035A-5 (1-1254) x JQ0405 (1-1106)	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similarity: 27.7% Query Match: DB: A.59-07 Length: Matches: 157 Conservative: 19 Mismatches: 183 Query Match: 10.4% Indels: 29	A; Accession: JUT405 A; Molecule type: DNA A; Residues: 1-1106 <shi> A; Residues: 1-1106 <shi> A; Cross-references: UNIPARC: UPI0000177394; EMBL: X15867 A; Cross-references: UNIPARC: UPI0000177394; EMBL: X15867 A; Mote: this reading frame extends between two stop codons and does not begin with a sta A; Mote: the gene encoding this protein overlaps uvrA gene C; Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;</shi></shi>	C:Species: Micrococcus luteus, Micrococcus lysodeikticus C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 04-Feb-2000 C:Accession: JQ0405 C:Accession: JQ0405 R:Shiota, S.; Nakayama, H. Mol. Gen. Genet. 217, 332-340, 1989 A;Title: Micrococcus luteus homolog of the Escherichia coli uvrA gene: identification of A;Reference number: S04781; MUID:89364717; PMID:2549377	Db 417 ArgGluIleAlaSerGluProValAlaGluHisTyrPheTyrThrAlaAsp 433 RESULT 10 JQ0405 hypothetical 119.5K protein (uvrA region) - Micrococcus luteus	397 LysaspLeuGlypheArgMetPheAlaValGlyValGlyAsnAlaValGluAspG 535 TCAGCCGCTGCAGCCCCTGCCGAGAAGCACCTGCACTTTGTGGACGTGGAT	Qy 415 CTGGTGTGGGTGACAGATGGCGGCTCCAGCGACCCTGTGGGCCCCCATGCAGGAGCTC 474	Qy 355 TATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCAGGGGTGCCCAAAGTG 414	Qy 295 GATGCGGTGCTTCTGCCCAGGGCATGGGTGACACCCACACTGGCCTGGTC 354	Qy 235 GGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGCTCGGGTGAGGCTGGCCCAG 294	Oy 175 CAGCTGGTGGCTCCACTGCCCCTGGGCACCGGGGGCCCTGCGTGCCAGTCTGGTGCACGTG 234 :::	OY 115 CTGGACAGCTCAGCGAGCGTCTCCACTACGAGTTCTCCCGGGTTTCGGGGAGTTTGTGGGG 174 :::	Oy 73 GGTCCACCAGCATCAGCCCCCCGAGGGGACCTGATGTTCCTG 114	Gaps: 3809 (1-493)	Score: 248.50 Matches: 66 Percent Similarity: 49.4% Conservative: 22 Best Local Similarity: 37.1% Minatches: 83 Conservation: 7
Qy	\$ \$ \$ \$	0y 0y 0b 0b	D Q D Q	D	אַ אַ	Qy Qy	Db Qy	Qy Db	Qy Db	Db Qy	Qy Db	Db Qy	Db Oy	D Qy
681 CCGCCTGGCCTGGCCACCCCTGCTGACCGCAGACTCGGGCTACTATGTGCT 731	641 641 868 ArgGlyValProArgGlyProValGlnProGlyAspAlaArgGlyHisLeuGlnGlyGln 887 642GCAGCAGCTCCATGCCACGGAGATCAC	582 CGTGGATGACCTGCACATCATTGTCCAAAGAGCTGAGGGGCTC 623	462 CATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGAGGCAA 521	748 ArgLeuArgGinValHisAlaAspGinArgAspProLeuGinGlyProGlyGinProAla 767 444GGCCCCCGTGT	CGGCTCCAGProAlaArgGlyProHisGlyArgAspGlyArgVal	333CACACTGGCCTGGCGCTGGTCTATGCCAAGGAACAGCTGTT 374	285 GGCTGCCAGGATGCGGTGCGTGCTTCTGCCCAGCGCATGGGTGACAC 332	234GGGCAGTCGGCCATACACCGAGTTCCCCTTCGGCCAGCACAGCTCGGGTGA 284 ::: ::: :::	233 233 666 ArgProSerArgGlyArgValArgArgArgGlyArgAlaLeuGlyLeuProGlyGlySer 685	233 233 646 ProHisArgArgAlaArgArgGlyHisAspArgArgGlyGlyLeuAspArgGlyHis 665	180 GGTGGCTCCACTGCCCCTGGGGACCGGGGCCCTGCGTGCCAGTCTGGTGCACGT 233	126 AGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTTCGGGGAGTTTGTGGGGCAGCT 179	72 CGGTCCACCAGCATCAGCCCCCCGAGGGGACCTGATGTTCCTGCTGGACAGCTC 125 :::	24 CCTGGCCCTGAGCTTGCGGCTGGCGCTGGCGCGGAGCGGCGCGGAGCG 71 569 ProGlyProAlaGlyValProAlaGlyArgArgProArgValProGlnPro 585

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A;Molecule type: mRNA
A;Residues: 1-500 <ASZ>
A;Cross-references: UNIPROT:P51942; UNIPARC:UPI0000029480; EMBL:U35035
A;Genetics:
A;Gene: CMP
C;Superfamily: cartilage matrix protein; EGF homology; von Willebrand
F;1-29/Domain: signal sequence #status predicted <SIG-
F;30-500/Product: cartilage matrix protein #sratus predicted <MAT-
F;43-210/Domain: von Willebrand factor type A repeat homology <VWA1-
F;231-266/Domain: EGF homology <EGF-
                                                                                                                                                                                                                                                                                                                                          cartilage matrix protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S66522
R;Aszodi, A.; Hauser, N.; Studer, D.; Paulsson, M.; Hiripi, L.; Bosze, Z.
Biochem. 236, 970-977, 1996
                                                                                                                                                                                                                                                                                              Eur. J. Biochem. 236, 970-977, 1996
A;Title: Cloning, sequencing and expression analysis of
A;Reference number: S66522; MUID:96270751; PMID:8665920
A;Accession: S66522
              Percent Similarity:
Best Local Similarity:
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A;Cross-references: UNIPROT:P03181; UNIPARC:UPI000000CDC0 R;Baer, R.; Bankler, A.T.; Biggin, M.D.; Deininger, P.L.; Farre Nature 310, 207-211, 1984
A;Title: DNA sequence and expression of the B95-8 Epstein-Barr A;Reference number: A03794; MUID:84270667; PMID:6087149
                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, Mol. Biol. Med. 1, 21-45, 1983
A;Title: Sequence analysis of the 17,166 bp EcoRI fragmen A;Reference number: A93065; MUID:85035713; PMID:6092825
A;Accession: A03742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: human herpesvirus 4, Epstein-Barr virus C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 (2,Accession: A03742)
                                                                                                                                                                                                                  A;Contents: annotation; protein coding region C;Comment: The sequence contains four perfect repeats C;Superfamily: human herpesvirus 4 BHLF1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12

QQBE3

BHLF1 protein - human herpesvirus 4 (strain B95-8)
                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-660 <BJ
US-10-699-035A-5 (1-1254) x QQBE3 (1-660)
                                                                                                                                                                         Alignment
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                                                                                                                                                       No
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A;Experimental source: splice form B A;Experimental source: splice form B A;Note: GenBank entries HMWEPISIB1 and HUWEPISIB2 present only the amino-and carboxyl-en R;Gendler, S.J.; Liancaster, C.A.; Taylor-Papadimitriou, J.; Duhig, T.; Peat, N.; Burchel J. Biol. Chem. 265, 15286-15293, 1990 J. Biol. Chem. 265, 15286-15293, 1990 A;Reference number: A35886; MUID:90368715; PMID:1697589 A;Recession: A35886 A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-19,29-992,1033-1344 <gen- 15294-15299,="" 1990="" 265,="" a35887;="" a;reference="" a;rote:="" batta,="" biol.="" chem.="" copy="" entry="" genbank="" hollingsworth,="" hummucab="" includes="" j.="" m.a.="" m.s.;="" muid:90368716;="" number:="" of="" one="" pmid:2394722<="" qî,="" r.s.;="" r;lan,="" repeated="" s.k.;="" sequence="" tandemly="" td="" the="" w.n.;="" wetzgar,=""><td>L.; Vos, H.L.; Gennissen, A.M.C.; Hikens, J. 5, 5573-5578, 1990 6, a carcinoma-associated mucin, is generated by a polymorphic gene real and the state of the s</td><td>Qy 40 GCAAGCTCAAGGCCAAGCCGTCCAAGGGAAGCA 2 </td><td>501 GLY 175 GCC 521 Cys 118 CCA 541 Gln 85 ATG 85 ATG</td><td>427 ArgProSerGlyProThrGlyGlyArgProAlaAlaProGlyAlaProGlyThrPro 307 CACGCACCGCATCCTGGG</td></gen->	L.; Vos, H.L.; Gennissen, A.M.C.; Hikens, J. 5, 5573-5578, 1990 6, a carcinoma-associated mucin, is generated by a polymorphic gene real and the state of the s	Qy 40 GCAAGCTCAAGGCCAAGCCGTCCAAGGGAAGCA 2	501 GLY 175 GCC 521 Cys 118 CCA 541 Gln 85 ATG 85 ATG	427 ArgProSerGlyProThrGlyGlyArgProAlaAlaProGlyAlaProGlyThrPro 307 CACGCACCGCATCCTGGG

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submitted to the EMBL Data Library, March 1990

A;Reference number: $40293

A;Accession: $40293

A;Accession: $40293

A;Molecule type: mRNA

A;Residues: 1-19,29-155,'P',157-175,'P',177-182,'A',184-212,1033-1037,'A',1039-1344 <WR2

A;Cross-references: UNIPARC::UPIO00016B0A6; EMBL:X52229; NID:g37053; PIDN:CAA36478.1; PID

R;Abe, M.; $iddiqui, J.; Kufe, D.

Biochem. Biophys. Res. Commun. 165, 644-649, 1989

A;Title: Sequence analysis of the 5' region of the human DF3 breast carcinoma-associated A;Reference number: A36735; MUID:90088473; PMID:2597151

A;Accession: A36735

A;Accession: A36735

A;Cross-references: UNIPARC::UPI000017456A; EMBL:M31823; NID:g181542; PIDN:AAA35757.1; PI

R;Masuzawa, Y.; Miyauchi, T.; Hamanoue, M.; Ando, S.; Yoshida, J.; Takao, S.; Shimazu, H

J. Biochem. 112, 609-615, 1992

A;Title: A novel core protein as well as polymorphic epithelial mucin carry peanut agglu

A;Reference number: JX0235; MUID:93123189; PMID:1478919
                                                                                                                                                                                                                                                           A;Gene: GDB:MUC1; PUM
A;Gross-references: GDB:120705; OMIM:158340
A;Cross-references: GDB:120705; OMIM:158340
A;Cross-references: GDB:120705; DMIM:158340
A;Map position: 1q21-1q23
A;Introns: 20/1; 62/3; 1165/3; 1184/2; 1230/1; 1270/3; 1320/3
C;Superfamily: polymorphic epithelial mucin
C;Keywords: alternative splicing; duplication; glycoprotein; phosphoprotein; polymorph
F;1-134/Product: mucin 1 precursor, splice form A #status predicted <PREA>
F;1-62/Region: mucin 1 amino-terminal non-repetitive
F;1-23/Domain: signal sequence #link PREA #status predicted <SIGB>
F;1-19,29-32/Domain: signal sequence #link PREB #status predicted <SIGB>
F;1-19,29-32/Domain: signal sequence #link PREB #status predicted <SIGB>
F;1-19,29-3144/Product: mucin 1 precursor, splice form B #status predicted <PREB>
F;138-1017/Region: 20-residue repeats (GSTAPPAHGVTSAPDTRPAP)
F;134-1272/Domain: transmembrane #status predicted <TRM>
F;1046,1064,1118,1144,1222/Binding site: carbobydrate (Asn) (covalent) #status predicted
F;1213/Binding site: phosphate (Tyr) (covalent) #status predicted
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A;Status: not compared with conceptual translation
A;Residues: 1-19,29-1109,'S',1111-1339,'A',1341-1344 <LAN>
A;Residues: 1-19,29-1109,'S',1111-1339,'A',1341-1344
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C;Comment: Serine and threonine residues in the tandem repeat domain are extensively gl C;Comment: For an alternative splice form without a tandem repeat domain, see PIR:S4814
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A;Residues: 1-19,29-155,'P',157-175,'P',177-182,'A',184-212,1033-1344
A;Cross-references: UNIPARC:UPI0000174569; EMBL:X52229; NID:g37053
R;Wreschner, D.H.
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A;Residues: 998-1011,'ES',1014-1017;1018-1032,'T',1034-1037;1038-1057 <MAS>
A;Cross-references: UNIPARC:UPI000017456B; UNIPARC:UPI000017456C; UNIPARC:UPI000017456D
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                                                                                      Percent Similarity:
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RESULT 14
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Query
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                                                                                                                                                                                                                                                   C;Superfamily: cartilage matrix protein; EGF homology; von C;Keywords: glycoprotein; homotrimer F;1-22/Domain: signal sequence #status predicted <SIG>
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A;Cross:referes: GDB:127280; OMIM:115437
A;Map position: 1p35-1p35
A;Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1; 481/1
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A;Residues: 157-290,'L',292-496 <JE2>
A;Cross-references: UNIPARC:UPI000016A6E8; GB:M55683;
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A;Title: Structure and chromosomal location of the human gene
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A;Introns: 30/1
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collagen alpha 3(VI) chain precursor - chicken
(;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Aug-2004
C;Accession: A37797; A34270; A32674
R;Doliana, R.; Bonaldo, P.; Colombatti, A.
J. Cell Biol. 111, 2197-2205, 1990
A;Title: Multiple forms of chicken alpha3(VI) collagen chain generated by alternat A;Reference number: A37797; MUID:91035630; PMID:1977751
A;Reference number: A37797; MUID:91035630; PMID:1977751
A;Accession: A37797
A;Molecule type: mRNA
A;Cross-references: UNIPROT:P15989; UNIPARC:UP10000173C31; UNIPARC:UP10000173C32;
A;Cross-references: UNIPROT:P15989; UNIPARC:UP10000173C31; UNIPARC:UP10000173C32;
                                                                                                         A;Title: The carboxyl terminus of the chicken alpha3 chain A;Reference number: A32674; MUID:90062147; PMID:2584214 A;Accession: A32674 A;Molecule type: mRNA A;Residues: 2151-219;2792-3137 <B02>
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                                                                                                                                                                                                                                                                    R;Bonaldo, P.; Colombatti, A.
J. Biol. Chem. 264, 20235-20239,
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A;Note: the authors translated the codon TTC for residue
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A; Residues: 224-2871 <BON>
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                                                                                      A; Cross-references: UNIPARC: UPI0000173C39; UNIPARC: UPI0000173C3A;
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C;Keywords: alternative splicing; cell binding; coiled coil; connective tissue; extracel F;1-25/Domain: signal sequence #status predicted <SIG>F;26-3137/Product: collagen alpha 3(VI) Chain #status predicted <MAT>F;26-2042/Domain: con-collagenous #status predicted <NNC>F;26-2042/Domain: von Willebrand factor type A repeat homology <VW01>F;36-202/Domain: von Willebrand factor type A repeat homology <VW02>F;442-607/Domain: von Willebrand factor type A repeat homology <VW04>F;8407-1004/Domain: von Willebrand factor type A repeat homology <VW06>F;1033-1197/Domain: von Willebrand factor type A repeat homology <VW07>F;1039-1197/Domain: von Willebrand factor type A repeat homology <VW07>F;1439-1604/Domain: von Willebrand factor type A repeat homology <VW07>F;1439-1604/Domain: von Willebrand factor type A repeat homology <VW07>F;1439-1804/Domain: von Willebrand factor type A repeat homology <VW07>F;1838-2010/Domain: von Willebrand factor type A repeat homology <VW09>F;1839-21804/Domain: von Willebrand factor type A repeat homology <VW09>F;1839-21804/Pregion: cell attachment (R-G-D) motif F;2015-2155/Region: cell attachment (R-G-D) motif F;2159-2161/Region: cell attachment (R-G-D) motif F;2159-2161/Region: cell attachment (R-G-D) motif F;230-2806/Domain: von Willebrand factor type A repeat homology <VW11>F;2623-2806/Domain: von Willebrand factor type A repeat homology <VW12>F;2630-2806/Domain: von Willebrand factor type A repeat homology <VW12>F;2630-2806/Domain: von Willebrand factor type A repeat homology <VW12>F;2630-2806/Domain: on Willebrand factor type A repeat homology <WW12>F;263-2303/Domain: on Willebrand factor type A repeat homology <WW12>F;2630-2806/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>F;201,2084,2436,2563,2581,2683,2867,2920,3003/Binding site: carbohydrate (Asn) (covalent
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                                                 SerSerValLeuLysSerAlaHisValAsnMetIleAlaValGlyValGlnAspAlaVal 180
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  TTCCTGGAGCTGTCAGCCGCTGCCTAGCCCCTGCCGAGAAGCACCTG---CACTTTGTG
                                                                                                   ATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGAGGCAAC
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                                                                                                                                                                                                                                                                                                               CTGGTCTATGCCAAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCCGG-----CCAGGG 402
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Search completed: February 13, 2006, 13:41:49 Job time: 78.062 secs

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Result
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-MODEL-frame+ n2p.model -DEV=xlp
-Q=/abss/ABSSWEB spool/US10699035/runat 13022006_062441_25416/app_query.fasta_1
-Q=/abss/ABSSWEB spool/US10699035/runat 13022006_062441_25416/app_query.fasta_1
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINNATCH=0.1 -LOOPCL=0 -LOOPEXY=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALICN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALICN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs802p
-USER=US10699035 @CCN 1 1_580 @runat 13022006 062441 25416 -NCPU=6 -ICPU=3
-NO MAAP -NEG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -KARAPOP=10 -KARPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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2: uniprot_trembl:*
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Fgapop 6.0 , F
Delop 6.0 , F
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Q8R2Z5_MOUSE
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11.9	11.9	11.9	11.9	12.0	12.1	12.1	12.2		13.1	13.3	13.5	13.6	13.6	14.3	14.9	15.2	15.7	15.9	16.1	16.2	16.3	16.3	16.3	16.3	16.3	16.3	16.5	16.5
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NUCLEOTIDE SEQUENCE.	c. Natl	and mouse cDNA sequences.";	S.J.M., Marra M.A.;	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		G.G.,	Vilialon ש.א., muzny ש.א., sodergren ש.ט., שנו א., Glods א.א., Sanchez A., Fahev J., Helton E., Ketteman M., Madan A., Rodriques S., Sanchez A.,	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	.D., Mullahy	J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	Soares M.B., Bonaldo M.F., Casavant T.L., S	in G.M., I	Jordan H., Moore T., Max S.I., Wang J., Hsieh	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		NUCLEOTIDE SEQUENCE.		NORT THATTH-0606.	bacecontal acatomorphisms, entimaced, encattering	Mammalia: Rutheria: Ruarchontodiires: Drimates: Catarrhini: Hominidae:		P4-758J18.11-001;	Von Willebrand factor A domain-related protein, isoform 1 (WARP).	(TrEMBLrel. 31, Last annota	(TrEMBLrel, 27,	2004 (TrEMBLrel.			IIT 1

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InterPro; IPR003961; FN III.

InterPro; IPR002035; VWF_A.

Pfam; PF00041; fn3; 2.

Pfam; PF00092; VWA; 1.

PRINTS; PR00433; VWFDOMAIN.

SMART; SM00060; FN3; 2.

SMART; SM000327; VWA; 1.

PROSITE; PS50234; VWFA; 1.

PROSITE; PS50234; VWFA; 1.

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ATTGTCCAAGAGCTGAGGGGCTCCATTCTC--
                             AlaAlaSerAlaProAlaGluLysHisLeuHisPheValAspVal
                                      GCTGCCTCAGCCCCTGCCGAGAAGCACCTGCACTTTGTGGACGTGGATGACCTGCACATC
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Von Willebrand factor A domain-related protein (Mus musculus 11 d
pregnant adult female ovary and uterus cDNA, RIKEN full-length
enriched library, clone:5031410I23 product:VON WILLEBRAND FACTOR
RELATED PROTEIN homolog).
 TISSUE=Colon, and Mammary tumor metastatized MEDLINE=22388257; PubMed=12
                             NUCLEOTIDE SEQUENCE.
STRAIN=Czech II, and
                                                                                                 Mus musculus (Mouse)
                                                                                                            Name=Vwa1
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   pubMed=12477932;
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
br. 199116899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II
"Analysis of the mouse transcriptome based on functional
60,770 full-length cDNAs.";
Nature 420:563-573(2002)
                                      STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDN
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P. Hayvashizaki V.;
"High-efficiency full-length cDNA cloning.";
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"Functional annotation of
Nature 409:685-690(2001).
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genes.";
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STRAIN=C57BL/6J; TISSUE=Ovary and uterus;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hirantoto K., Hiraoka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Katoh H., Somura K., Numazaki R., Ohno M., Obsato N., Okazaki Y.,

RA Nishi K., Nomura K., Numazaki R., Ohno M., Obsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

RA Tagawa A., Takahus Akahira S., Takeda Y., Tanaka T.,

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M.

IN 101

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MEDLINB=20530913; PLbMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

KONNO H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000)
                                                                                                                                                                                                                                                                                                                                      Local
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GO; GO:0005615;
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EMBL; AK077240; BAC36703.1;
EMBL; BC036166; AAH36166.1;
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Director MGC Project;
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PROSITE; PS50234; VWFA; 1
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PF00092; VWA; 1
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                       AGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTTTCGGGAGTTTGTGGGGGCAGCTG
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IPR003961; FN III.
IPR002035; VWF_A.
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LeuGlyProLeuGlnGlyGlySerLeuGluArgValGluValProAlaGlyGlnAsnSer
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O221X3 MOUSE PRELIMINARY; PRT; 415 AA.

ID O221X3 MOUSE PRELIMINARY; PRT; 415 AA.

O221X3

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 19, Last sequence)

DT 01-MAR-2004 (TrEMBLrel. 19, Last sequence)

DT 01-MAR-2004 (TrEMBLrel. 19, Last sequence)

DE von willebrand factor A-related protein.

Name=vwal; Synonyms=4932416A11Rik, Warp;

Mus musculus (Mouse).

CE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

CM musculus (Mouse).

CM Mammalia; Butheria; Buarchontogiires; Glires; Rodentia; Sciurognathi;

CM Mammalia; Butheria; Buarchontogiires; Glires; Rodentia; Sciurognathi;

CM MCDITIDE SEQUENCE.

RP MUCLEOTIDE SEQUENCE.

RP MUCLEOTIDE SEQUENCE.

RP MUCLEOTIDE SEQUENCE.

RP FILTOGRAPH AND ST., Bateman J.F.;

"WARP a new member of the von Willebrand factor A-domain superfamily

of extracellular matrix proceins.";

FEBS Lett. 517:61-66(2002).

RR FILTOGRAPH AND ST., MAR MUSCULUS.

RM MSS; PLBG14; NMFP

EMBEL; AYO30094; AAX38350.1; -; mRNA.

DR MSS; PLBG14; NMFP

EMSembl; ENSMUSG00000042116; Mus musculus.

MG1; MG1:2179729; 493416A11Rik.

DR G0; G00:005615; C:extracellular space; TAS.

DR InterPro; IPR00305; VWFA

DR FRINTS; PR0045; VWFA

DR FRINTS; PR0045; VWFA

DR PRINTS; PR0045; VWFA

DR SMART; SM00127; VWA; 1.

DR SMART; SM00127; VWA; 1.

DR PROSTITE; PS5083; FN III

DR PROSTITE; P
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Q8COQ7;
                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN fill-length (library, clone:4932416A11 product:VON WILLEBRAND FACTOR PROTEIN homolog.
       Name=Vwa1; S
Mus musculus
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              Synonyms=4932416A11Rik;
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RC STRAIN-C57BL/GJ; TISSUB=Testis;
RX MEDLINE-21085660; PubMed-11217851; DOI=10.1038/3505500;
RX MEDLINE-21085660; PubMed-11217851; DOI=10.1038/3505500;
RA ARAWA J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo M., Aono H., Baldarelli R., Barsh G.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Hyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashizaki Y., J.
                                                                                                                                                                                                                                                                                                  STRAIN-C57BL/6J; TISSUE-Testis;

MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

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Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
STRAIN=C57BL/6J; TISSUE=Testis;
Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carnii Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Testis; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cD prepare full-length cDNA libraries for rapid discovery of Genome Res. 10:1617-1630(2000).
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Nature 420:563-573(2002).
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Muroidea; Muridae; Murinae;
NCBI TaxID=10090;
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InterPro; IPR003961; FN III.
InterPro; IPR002035; VWF_A.
Pfam; PF00041; Kn3; 2.
Pfam; PF00041; Kn3; 2.
Pfam; PF000453; VWFADOMAIN.
SMART; SM00060; FN3; 2.
SMART; SM003027; VWA; 1.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50853; VWFA; 1.
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EMBL; AK030019; BAC26739.1; -; mRNA.

HSSP; P18614; 1MHP.
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Ensembl; ENSMUSG00000042116; Mus musculus.
MGI; MGI:2179729; 4932416A11Rik.
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MEDLINE 22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Piopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M.J., Ugdin T.B., Bonaldo M.F., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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46 RAT
Q642A6; RAT PRELIMINARY; PRT; 415 AA.
Q642A6;
Q5-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Von Willebrand factor A domain-related protein.
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurogna Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                         TISSUE=Kidney;
                                                                                                                                                    NUCLEOTIDE
                                                                                                                                                                                                                                         Name=RGD1311476
                                                                                                                                                                                                                           Rattus norvegicus (Rat).
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PÉAMI; PF00092; VWA; 1.
PRINTS; PR00453; VWFADOMAIN.
SMAAT; SM00060; FN3; 2.
SMAAT; SM00327; VWA; 1.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50854; VWFA; 1.
SEQUENCE 415 AA; 44832 MW;
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TISSUE=Kidn
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EMBL; BC081983; AAH81983.1;
InterPro; IPR003961; FN III.
InterPro; IPR002035; VWF A.
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            CTGGGCGTCACCGTGTTCATTGTCAGCACCGGCCGAGGCAACTTCCTGGAGCTGTCAGCC
                                             TGGGTGACAGATGGCGGCTCCAGCGACCCTGTGGGCCCCCCCATGCAGGAGCTCAAGGAC
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68.4%
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                                                                                                                                                                                                     Name=WAKr;
Homo sapiens (Human).
                                                                                                                                                                                                                             TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003543; AAH03543.2; -; mRNA.
InterPro; IPR003961; FN III.
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS50853; FN3; 1.
PROSITE; PS50853; FN3; 2.
NON TER
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SEQÜENCE 281 AA; 29628 MW; 350CCE4590791BD4 CRC64;
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                          AlaAlaLeuProAlaProGluGluAlaGlyProGluArgIleValIleSerHisAlaArg
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                                                                                    GluAlaGlyProGlyAlaSerGlyProGluSerGlyAlaGlyProAlaProThrGlnLeu
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Best Local Similarity:
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Ensembl; ENSG0000179403; Homo s.
InterPro; IPR003961; FN_III.
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS50853; FN3; 2.
SEQUENCE 233 AA; 24473 MW; B:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Hypothetical protein FLJ22215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watanabe K., Kumagai A., Itakura S.,
Suzuki Y., Obayashi M., Nishi T., Shi
Suzuki Y., Isogai T., Sugano S.;
Submitted (AUG-2000) to the EMBL/Geni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homin
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Q9H6J5;
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"Generation and initial sanitation of force than 18 no. full locath human in the One fell locath h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBVDV9 MOUSE PRELIMINARY;
QBVDV9 QBVDV9 (TrEMBLrel 2
01-MAR-2002 (TrEMBLrel 2
01-MAR-2004 (TrEMBLrel 2
4932416A11Rik protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Vwal; Synonyms=4932416AllRik; Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously, MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Czech
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Ensembl; BNSMUSG00000042116; Mus musculus.
MGI; MGI:2179729; 4932416A11Rik.
MGI; MGI:2179729; Vwal.
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR003961; FN_III.
pfam; pF00041; ff3; 2.
SMART; SM00060; FN3; 2.
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Proc. Natl. Acad. Sci. U.S.A.
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RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

RA Mauceli E., Bouneau L., Fischer S., Lutfalla G., Dossat C., Segurens B.,

RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

RA Anthouard V., Jubin C., Castella V., Katinka M., Vacherie B.,

RA Anthouard V., Jubin C., Castella V., Katinka M., Vacherie B.,

RA Aliemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,

RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

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RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lindblad-Toh K., Lander E.S., Weissenbach J., Roest Crollius H.;

Ra Lindblad-Toh K., Lander E
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Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoreleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whi
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF14659, whole genome shotgun sequence.
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      Archosauria; Aves; Gallus.
                                                                                          Name=COL12A1;
Gallus gallus (Chicken)
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MEDLINE=95370352; PubMed=7642694; DOI=10.1083/jcb.130.4.1005; Koch M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet M "Large and small splice variants of collagen XII: differential expression and ligand binding.";
J. Cell Biol. 130:1065-1014(1995).
-i- FUNCTION: Type XII collagen interacts with type I collagen-containing fibrils, the COLI domain could be associated with the surface of the fibrils, and the COL2 and NC3 domains may be localized in the perifibrilar matrix.
-i- SUBUNIT: Trimer of identical chains each containing 190 kDa of nontriple-helical sequences.
-i- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Embryo;

MEDLINE-93042014; PubMed=1420368; DOI=10.1016/0167-4781(92)90145-P;

Trueb J., Trueb B.;

"The two splice variants of collagen XII share a common 5' end.";

Biochim. Biophys. Acta 1171:97-98(1992).
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MEDLINE=92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209;
Yamagata M., Yamada K.M., Yamada S.S., Shinomura T., Tanaka H.,
Nishida Y., Obara M., Kimata K.;
"The complete primary structure of type XII collagen shows a chimeric
molecule with reiterated fibronectin type III motifs, von Willebrand
factor A motifs, a domain homologous to a noncollagenous region of
type IX collagen, and short collagenous domains with an Arg-Gly-Asp
site.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
MEDLINE=87317590; Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 264:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gordon M.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Type XII collagen. A large multidomain to type TX collagen.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gordon M.K., Gerecke D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90062079; PubMed=2584192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE
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unit
PTM:
(By 8
                                                                                                                                                                                                                                                                                          Name=Short;
IsoId=P13944-2; Sequence=VSP 001148;
TISSUE SPECIFICITY: Type XII collagen is present in tendons,
                                                                                                                                                          ligaments, perichondrium, and periosteum, all dense tissues containing type I collagen.

DOMAIN: This sequence defines five distinct domains, helical domains (COL1 and COL2) and three nontriple-domains (NC1, NC2, and NC3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
Comment=The final tissue form of collagen XII may contain
homotrimers of either isoform Long or isoform Short or any
combination of isoform Long and isoform Short. Only isoform Long
is a proteoglycan. Isoform Long has more restricted expression
     SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P13944-1; Sequence=Displayed;
                                similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cloning.";
                                                 Prolines at the third position of the tripeptide repeating (G-X-Y) are hydroxylated in some or all of the chains. O-glycosylated; glycosaminoglycan of chondroitin-sulfate to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  embryonic tissue
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Gerecke D.R., Olsen B.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264:19772-19778(1989)
Belongs to
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in molecule with partial homology
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EMBL; D00824; BAA00701.1; -; m

EMBL; X61024; CAA43358 1; -; m

EMBL; M17375; AAA48718 1; -; m

EMBL; J05137; AAA48635 1; -; m

EMBL; X67327; CAA47744.1; -; m

EMBL; X67320; A40020.
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SWART; SM00060; FN3; 18.
SWART; SM00210; TSPN; 11.
SWART; SM00327; VWA; 4.
PROSITE; PS50853; FN3; 18.
PROSITE; PS50853; FN3; 18.
Alternative splicing; Cell adhesion; Collagen;
Alternative splicing; Cell adhesion; Collagen;
Direct protein sequencing; Extracellular matrix;
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IPR003129; Laminin_G_TSP_N.
IPR002035; VWF_A.
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N-linked (GlcNAc
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                                                                                                ThrValGluAspPheAspAlaPheGlnArgIleSerPheGluLeuThrGlnSerValCys
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AsnThrGlyLysAlaMetThrTyrValArgGluLysValPheValThrSerLysGlySer
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    S (in Ref. 4).
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01-FEB-2005 (TrEMBLrel. 31, Le
13-SEP-2005 (TrEMBLrel. 31, Le
COllagen, type XII, alpha 1.
Name=COL12A1; ORFNames=RP1-238
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Euarchonto
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EMBL; AL096771; CAI19897.1; JOINED; Genomic_DNA.
EMBL; BIGG00000111799; Homo sapiens.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:000578; C:extracellular matrix (sensu Metazoa); IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
GO; GO:0007157; P:phosphate transport; IEA.
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PROSITE; PS50234; VWFA; 4.
Collagen; Extracellular matrix;
SEQUENCE 2884 AA; 315869 MW;
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InterPro; IPR003035; VWF_A.
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ EMBL; AL354664; CAH71310.1; -; Genomic_DNA. EMBL; AL080250; CAI19898.1; -; Genomic_DNA.
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Collagen, type XII, alpha 1.
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Name=COL12A; ORFWames=RP1-238D15.1-001;
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R GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.

R GO; GO:0005198; F:structural molecule activity; IEA.

R GO; GO:0007155; P:cell adhesion; IEA.

R GO; GO:0006817; P:phosphate transport; IEA.

R InterPro; IPR003961; FN III.

R InterPro; IPR003961; FN III.

R InterPro; IPR003129; Laminin G TSP_N.

R InterPro; IPR002035; VWF_A.

R Pfam; PF0191; Collagen; 4.

R Pfam; PF0191; Collagen; 4.

R Pfam; PF00041; fn3; 18.

R Pfam; PF00041; fn3; 18.

R PFANT; SM00307; VWA; 4.

R PROSITE; PS00853; FN3; 18.

R PROSITE; PS50853; FN3; 18.

R PROSITE; PS50853; FN3; 18.

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IL; AL096771; CAH71310.1; JOINED; Genomic_DNA.
IL; AL354664; CAI19898.1; JOINED; Genomic_DNA.
II; AL080250; CAI19908.1; JOINED; Genomic_DNA.
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MEDLINE=97288521; PubMed=9143499; DOI=10.1006/geno.1997.4638; Gerecke D.R., Olson P.F., Koch M., Knoll J.H.M., Taylor R., Hudson D.L., Champliaud M.-F., Olson B.R., Burgeson R.E.; "Complete primary structure of two splice variants of collagen and assignment of alpha 1(XII) collagen (COL12A1), alpha 1(IX) collagen (COL19A1) to human
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
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                                                                                                                                                                                                                                         (ISOFORMS LONG
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InterPro; IPRO08160; Collagen.
InterPro; IPRO03961; VWF III.
InterPro; IPRO0395; VWF A.
Pfam; PF01391; Collagen; 4.
Pfam; PF00092; VWA; 4.
PRINTS; PRO0453; VWFADOMAIN.
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-i- FUNCTION: Type XII collagen interacts with type I collagen-containing fibrils, the COL1 domain could be associated with the surface of the fibrils, and the COL2 and NC3 domains may be localized in the perifibrillar matrix (By similarity).

-i- SUBUNIT: Trimer of identical chains each containing 190 kDa of nontriple-helical sequences.

-i- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms-2;
Comment-The final tissue form of collagen XII may contain homotrimers of either isoform Long or isoform Short or any combination of isoform Long and isoform Short;
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                                                                                                                                  Alternative splicing; Cell adhesion; Direct protein sequencing; Extracell, Hydroxylation; Repeat; Signal; Struct SIGNAL 25 3063 Collage:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                              PROSITE; PS50853; FN3; 18. PROSITE; PS50234; VWFA; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unit (G-X-Y) are hydroxylated in some or all of the chains similarity).

PTM: O-glycosylation of isoform Long; glycosaminoglycan chondroitin-sulfate type (By similarity).

SIMILARITY: Belongs to the fibril-associated collagens winterrupted helices (FACIT) family.

SIMILARITY: Contains 18 fibronectin type-III domains.

SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.

SIMILARITY: Contains 4 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                   GO:0005595; C:collagen type XII; TAS. GO:0001501; P:skeletal development; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: The triple-helical tail is stabilized each end (By similarity).

PTM: Prolines at the third position of the unit (G-X-Y) are hydroxylated in some or al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q99715-2; Sequence=VSP 001149; TISSUE SPECIFICITY: Found in collapse 1 containing tissues: both isoform Short and isoform Long appear in amnion, chorion, skeleta muscle, small intestine, and in cell culture of dermal fibroblasts, keratinocytes and endothelial cells. Only the short isoform is found in lung, placenta, kidney and a squamous cell carcinoma cell line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Short;
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                                                                                                                                                          sequencing; Extracellular matrix; Glycoprotein; Repeat; Signal; Structural protein
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                                CGGGTTCGGGAGTTTGTGGGGCAGCTGGTGGCTCCACTGCCCCTGGGCACCGGGGCCCTG
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An Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
An Nicaud S., Salanoubat M., Levy M., Boudet N., Castellano S.,
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Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
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Anthouard C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
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A Rellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
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"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
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PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00060; FN3; 11.
SMART; SM00327; VWA; 3.
PROSITE; PS50853; FN3; 12.
PROSITE; PS50234; VWFA; 3.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 14 SCAF14645, whole genome shotgun seque
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Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whi
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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InterPro; IPR003961; FNIII subd.
InterPro; IPR003962; FNIII subd.
InterPro; IPR003035; VWF_A.
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 CACGTGCAGTTCGGGCCGCTGCGGGGGGGGGGGGGCGCGCGGGTGGAGGTGCCCGCGGGC
                                                                                                                                                                                                      GACTACGACGTGCCTAGTGCCTGAGTCCAACGTGCGCCTCCTGAGGCCCCAGATCCTG
                                                                                                                                                                                                                                    SerMetSerValProGlyAspValLeuThrAlaLeuLeuProHisLeuThrProLeuThr
                                                                                                                                                                                                                                                                                                       AsnValGluSerTyrLeuValGlnPheArgProThrGluGlyGluAspSerHisTyrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuArgIleGluGlnGluLeuGlnIleIleAsnGlnArgArgLeuValGlnProArgAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AspAlaValArgSerGluLeuGluAlaIleAlaAsnAlaProAlaGluThrHisValTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlnGluProAlaAlaAsnLeuArgAsnSerAspValGluIlePheAlaValGlyValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCCCCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgAlaHisValProArgValThrIleLeuIleThrAspGlyLysSerSerAspAlaPhe
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                               ProGlnSerPheArgValSerTrpArgAlaAlaProGlyAlaValAlaArg-----Tyr
                                                                 TyrGlyThrThrAlaGluGluArgGlySerValGlnAsnLeuLysValThrGluGluSer
                                                                                                                                  CGGGTGCGCACGCCGAGAGGAGGCCGGGCCAGAGCGCATCGTCATCTCCCACGCCCGG
                                                                                                                                                                                                                                                                      GCAGACTCGGGCTACTATGTGCTGGAGCTGGTGCCCAGCGCCCAGCCGGGGGCTGCAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COCA1 MOUSE STANDARD; PI
Q60847; P70322;
15-JUL-1998 (Rel. 36, Created)
28-FEB-2003 (Rel. 41, Last seque
10-MAY-2005 (Rel. 47, Last annot
Collagen alpha 1(XII) chain pree
                                                                                                                                                                                                                                                                                                                              "Structural variation of type XII collagen at its carboxyl-terminal NC1 domain generated by tissue-specific alternative splicing.";
J. Biol. Chem. 274:22053-22059(1999).
-i- FUNCTION: Type XII collagen interacts with type I collagen containing fibrils, the COL1 domain could be associated with the surface of the fibrils, and the COL2 and NC3 domains may be localized in the perifibrillar matrix (By similarity).
-i- SUBUNIT: Trimer of identical chains each containing 190 kDa of nontriple-helical sequences (By similarity).
-i- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99348349; PubMed=10419532; DOI=10.1074/jbc.274.31.22053; Kania A.M., Reichenberger E., Baur S.T., Karimbux N.Y., Taylor R Olsen B.R., Nishimura I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96170761; PubMed=8601036;
Boehme K., Li Y., Oh P.S., Olsen B.R.;
"Primary structure of the long and short splice variants
collagen XII and their tissue-specific expression during
development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniat;
Mammalia; Eutheria; Euarchontoglires;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Coll2al;
Mus musculus (Mouse)
                                                                            -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND XIIB-2).
STRAIN=C57BL/6J; TISSUE=Skin fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL NUCLEOTIDE SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J, and Swiss Webster;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XIIB-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE, AND ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUSE
ISOID-060847-4; Sequence=VSP_001150, VSP_001151, VSP_001152; TISOID-060847-4; Sequence=VSP_001150, VSP_001151, VSP_001152; TISOID-0608481, TISOID-0608481, TISOID-0608481, and periosteum. Skin, cornea, Scilera, blood vessels, and periosteum.

DEVELOPMENTAL STAGE: The long NC3 XIIA isoforms are predominant a early-stages (ED7 and 11); at later stages of development (ED15 and 17) the short NC3 XIIB forms become the major forms. As the short NC3 forms become the major product, the long splice variant continues to be expressed in several tissues, even after birth.
                                                                                                                                                                                                                                                                         Event-Alternative splicing; Named isoforms=4;
Event-Alternative splicing; Named isoforms=4;
Comment=The final tissue form of collagen XII may contain
Comment-rimers or any combination of the various isoforms;
                                                                                                                                                                                                Name=XIIA-2; Synonyms=ER#K;
IsoId=Q60847-2; Sequence=VSP_001151,
                                                                                                                                                                                       Name=XIIB-1
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                                                                                                                                                                IsoId=Q60847-3; Sequence=VSP_001150;
                                                                                                                                                                                                                                        IsoId=Q60847-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCGCCGCCTTCCGCTCGGGCCGCGAGAGCCGCCGCTGTCCGCCAAGGCCCTGCACGCCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProGluLeuThrMetValLeuGlnAspLeuGlnProArgThrThrTyrArgValThrVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence up
Last annotation
chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Skin;
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                                                                                                                                                                                                  VSP_001152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Taylor R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XIIA-1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of mouse
embryonic
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Pfam; PF00092; VwA; ...
Pfam; PF00092; VwA; ...
PRINTS; PR00453; VWFADOMAIN.
SWART; SM0060; FN3; 18.
SMART; SM00210; TSPN; 1.
SWART; SM00327; VWA; 4.
PROSITE; PS50853; FN3; 18.
PROSITE; PS50234; VWFA; 4.
Alternative splicing; Cell adhesion; Collagen; Extracellular matrix; Alternative splicing; Cell, adhesion; Signal; Structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U25652;
EMBL; U57095;
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similarity)
PTM: O-glyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MGI:88448;
GO:0005615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chondroitin-sulfate type (By similarity).

SIMILARITY: Belongs to the fibril-associated collagens with interrupted helices (FACIT) family.

SIMILARITY: Contains 18 fibronectin type-III domains.

SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.

SIMILARITY: Contains 4 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The long NC1 isoforms, XIIA-1 and XIIB-1, peak in 15-day old embryos and decrease in 17-day old ones. The expression of the short NC1 form XIIB-2 remains constant throughout late stages of embryonic development (ED15 and ED17).

PTM: The triple-helical tail is stabilized by disulfide bonds at each end (By similarity).

PTM: Prolines at the third position of the tripeptide repeating unit (G.X.-Y) are hydroxylated in some or all of the chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Swiss-Prot entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FuoT
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                                   as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bioinformatics Institute.
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AAB07047.1;
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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.
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February 13, 2006, 07:33:59; Search time 142.074 Seconds (without alignments) 893.868 Million cell updates/sec

Title:
Perfect score:
Sequence:

US-10-699-035A-2 913 1 RGDLMFLLDSSASVSHYEFS......FVDVDDLHIIVQELRGSILD 180

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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01-UN-2002 (TrEMBLrel. 21, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Von Willebrand factor A domain-related protein (Mus musculus 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriched library, clone:5031410123 product:VON WILLEBRAND FACTOR A-RELATED PROTEIN homolog).
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RAWAI J., Shinagawa A., Shibata K., Yoshibo M., Itoh M., Ishii Y., Ala Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M., A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., A Sasaki H., Sato K., Schoenbach C., Seya T., Shbata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Washaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muzamatsu M., Inoue Y., Kira A., Hayashizaki Y.;
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sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
STRAIN-C57BL/6J; TISSUE-Ovary and uterus;
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Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs t prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
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Best Local Sim:
Matches 151;
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InterPro; IPR002035; VWF A.
Pfam; PP00041; fin; 2.
Pfam; PP00092; VWA; 1.
PRINTS; PR00453; VWFADOWAIN.
SMART; SM00505; FN3; 2.
SMART; SM00327; VWA; 1.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50853; VWFA; 1.
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Tagawa A.,
Tomaru A.,
Submitted (
                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Von Willebrand factor A-related protein.
Name=Vwal; Synonyms=4932416AllRik, Warp;
                                                                               FEBS Lett. 517:61-66(2002).
EMBL; AY030094; AAK38350.1; -; mRNA.
HSSP; P18614; 1MHP.
                                                                                                                      MEDLINE=22057805; PubMed=12062410; DOI=10.1016/S0014-5793(02)02579-6; Fitzgerald J., Ting S.T., Bateman J.F.; Fitzgerald J., Ting S.T., Bateman J.F.; WARP a new member of the von Willebrand factor A-domain superfamily of extracellular matrix proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC026919; AAH26919.1;
EMBL; AK077240; BAC36703.1;
EMBL; BC036166; AAH36166.1;
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STRAIN=FVB/N; TISSUE=Colon;
Director MGC Project;
Submitted (JUL-2002) to the
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                            GO; GO:0005615;
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              InterPro;
sembl; ENSMUSG00000042116; Mus m
I; MGI:2179729; 4932416A11Rik.
I; MGI:2179729; Vwa1.
GO:0005615; C:extracellular sp
terPro; IPR003961; FN III.
terPro; IPR002035; VWF_A.
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GO:0005615; C:extracellular
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Muridae; Murinae;
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                                                                                                                                                                                                                                                              (Mouse)
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Euarchontoglires; Glires; Rodentia; Sciurogna
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Pred. No. 7.5e-60
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                                      A RAWAI J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Pfam; PF00092; VWA; 1.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00060; FN3; 2.
SMART; SM00377; VWA; 1.
R PROSITE; PS50853; FN3; 2.
R PROSITE; PS50234; VWFA; 1.
R PROSITE; PS50234; VWFA; 1.
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Best Local (
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01-MAR-2003 (TrEMBLrel 23, Last sequence update)
01-MAR-2004 (TrEMBLrel 26, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length (library, clone:4932416A11 product:VON WILLEBRAND FACTOR PROTEIN homolog.
                                                                                                                                                                                                                                                                                                                                                                                                   Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Testis; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636;
               Hayashizaki Y.; "Functional annotation
                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
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Mammalia; Eutheria; Euarchontoglires;
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Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hayashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Saasaki D., Shibata K., Shinagawa A., Takakathira S., Takeda Y., Tagami M
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUB=Testis;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                              GO; GO:0005615; C:extracellular InterPro; IPR003961; FN III. InterPro; IPR00395; VWF_A. Pfam; PF00041; fn3; 2. Pfam; PF00092; VWA; 1.
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i; MGI:2179729; Vwal.
GO:0005615; C:extracellular
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                                                                                                                                                                                                                         PS50853; FN3; 2.
PS50234; VWFA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                         ENSMUSG00000042116; Mus musculus.
                    SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVMVTDGGSSDPV
                                                          QGDLLFLLDSSASVSHYEFSRVREFVGQLVATMSFGPGALRASLVHVGSQPHTEFTFDQY
415
                                                                                                                                Conservative
                                                                                                                                                                                                        AA,
                                                                                                                                                                                                        44681 MW;
                                                                                                                                                 84.1%;
83.3%;
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                                                                                                                              Pred. No. 1.70
3; Mismatches
                                                                                                                                                                  Score 768;
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Ra Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Teneration and initial analysis of more than 15,000 full-length human property of the Marra M.A.;
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0453; VWFADOMAIN SMART; SM00060; FN3; 2. SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC081983; AAH81983.1; -; mRNA. InterPro; IPR003961; FN III. InterPro; IPR002035; VWF_A. PFAM. BENDAMING FOR THE PROPERTY OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation updat
Von Willebrand factor A domain-related protein.
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                  Local
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c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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PS50234; VWFA; 1
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                                SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
                                                                                                                                                           RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
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                                                                                                                       QGDLLFLLDSSASVSHYEFSRVREFVGQLVATMPFGPGALRASLVHVGSRPHTEFTFDQY
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                                                                                                                                                                                                                                                                                                                                                                             44832 MW;
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Pred. No. 7.1e-59;
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RESULT 7
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AC Q4SD22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORFNames=GSTENG00020556001;
Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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            Q4SD22 TETNG PRELIMINARY;
Q4SD22;
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NUCLEOTIDE SEQUENCE.

Genoscope; Whitehead Institute Centre for Genome Research;

Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an order of the control of the co
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13-SEP-2005 (TYEMBLrel. 31, Last sequence update)
13-SEP-2005 (TYEMBLrel. 31, Last annotation update)
13-SEP-2005 (TYEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF14659, whole genome sho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 397; DB 2;
Pred. No. 1.5e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            505
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γ
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RESULT 8
Q4SXE3_TETNG
ID Q4SXE3_TETNG
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SOUTH TANK TO DESCRIPT THE PROPERTY OF THE PRO
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RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Anthouard V., Jubin C., Castelli V., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Anthouard V., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McBwan P., Bosak S.,
RA Alindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";

Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collagen;
NON TER
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
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Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0014; FNTYPEIII.
PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00060; FN3; 11.
SMART; SM00327; VWA; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00041; fn3; 11. Pfam; PF00092; VWA; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope, Whitehead Institute Centre Submitted (FEB-2004) to the EMBL/GenBa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary data.; CAAE0101460.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nitted (FEB-2004) to the EMBL/GenBank/DDBJ da CAUTION: The sequence shown here is derived
                                                                                                                  496
                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                      l Similarity
67; Conserv
                                                                                                                                                                                                                                                                                              RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50853; FN3; 12.
PS50234; VWFA; 3.
                                                                                                               HILEAVVTALRTFPYRGGSTNTGRAMTYVRETVFQASRGARAHVPRVTILITDGKSSDAF
                                                                                                                                                                      SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 120
QEPAANLRNSDVEIFAVGVKDAVRSELEAIANAPAETHVYTVEDFDAFQRISTELTQSI
                                                    GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGSI 178
                                                                                                                                                                                                                                       QADVVLLVDGSYSIGLANFAKVRAFLEVLVNTFDIGPDKVQISLVQYSRDPHTEFYLDSH
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IPR003962; FnIII_s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Extracellular matrix;
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1723
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                                                                                                                                                                                                                                                                                                                                                                                  30.0%; Score 273.5; 37.4%; Pred. No. 5.2
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Last annotation update)
ole genome shotgun sequence.
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                                                                                                                                                                                                                                                                                                                                                                                     .2e-15;
                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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PRELIMINARY;

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Query
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InterPro; IPR008160; Collagen.
InterPro; IPR003961; FN_III.
InterPro; IPR003129; Laminin G_TSP_InterPro; IPR001220; Lectin_TegB.
InterPro; IPR002035; VWF A.
Pfam; PF001391; Collagen; 2.
Pfam; PF00041; fn3; 8.
Pfam; PF00092; VWA, 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak ?
Rellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Robinson-Rechavi I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laudet V., Schachter V., Quetier F., Saurin W., Robinson-Rechavi Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; "Genome duplication in the teleost fish Tetraodon nigroviridis rev the early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Ve
Actinopterygii; Neopterygii; Teleostei; Eu
Acanthomorpha; Acanthopterygii; Percomorph
Tetradontoidea; Tetraodontidae; Tetraodon.
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13-SEP-2005 (TrEMBLrel.
13-SEP-2005 (TrEMBLrel.
Chromosome undetermined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0453; VWFADOMAIN
SMART; SM00060; FN3; 9.
SMART; SM00210; TSPN; 1.
SMART; SM00327; VWA; 3.
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                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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[2]
                                                                                                                                                                                                                                                                                                                    ocal
                                                                                                                                                                                                                                                                                                                                             Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAUTION: The sequence she EMBL/GenBank/DDBJ whole preliminary data.
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                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS50853; FN3; 9.
PS00307; LECTIN_LEGUME_BETA; UNKNOWN
PS50234; VWFA; 3.
                                                                                                                                             GEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPVGP
                                                PMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHI---IVQELRGSIL
PAORLRDAGVEVFAIGVKNADEGELRAIASVSEDTHVY -- NVADFHLMADIVDVLTRTIC
                                                                                                KEAVMEAARNLPYKGGNTLTGLALTFILENSFSPESGSRPGIPKIGVLLTDGKSQDDVIP
                                                                                                                                                                                             DMVFLVDGSWSIGRTNFRLVRVFLESLVKAFDVDLDRTRIGLAQFSGEPRIEWHLNTHTT
                                                                                                                                                                                                                                           DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                           Extracellular
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                                                                                                                                                                                                                                                                                             Conservative
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31. Last sequence update)
31. Last annotation update)
SCAF12445, whole genome shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                         matrix; Structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           shown here is derived
                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                           Score 273.5; 1
Pred. No. 6.9e
28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome shotgun (WGS)
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                                                                                                                                                                                                                                                                                                                    No. 6.9
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Euteleostei;
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                                                                                                                                                                                                                                                                                           82;
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; Neoteleostei;
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COBA1_CHICK STANDARD P32018; Q6LBL0; 01-JUL-1993 (Rel. 26, C 01-OCT-1996 (Rel. 34, I 13-SEP-2005 (Rel. 48, I C Collagen alpha 1(XIV) c Name=COL1441;
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Q4RP12;
13-SEP-2005 (113-SEP-2005)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; l
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodo
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
.i- CAUTION: The sequence shown here is derived from an
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NUCLEOTIDE SEQUENCE.

Baillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot / Mauceli E., Bouneau L., Fischer S., Lutfalla G., Dossat C., Segun Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segun
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13-SEP-2005 (TrEMBLrel. 31, Last seque
13-SEP-2005 (TrEMBLrel. 31, Last annot
Chromosome 10 SCAF15009, whole genome
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36.3%;
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Trueb J., Trueb b.;
"Type XIV collagen is a variant of Fur. J. Biochem. 207:549-557(1992)
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van der Rest M., Mayne R., Olsen B.K.;
"Cloning of the cDNA for a new member of the class of fibril-
associated collagens with interrupted triple helices.";
Eur. J. Biochem. 201:333-338(1991).
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Eukaryota; Metazoa; Choruucu,
Eukaryota; Aves; Neognathae;
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MEDLINE=98357967; PubMed=9694594;
GITY-Lozinguez C., Aubert-Foucher
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van der Rest M., Mayne R., Olsen B.R.;
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MEDLINE=92037585; PubMed=1935930;
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MEDLINE=92339443; PubMed=1339349;
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                                                                                                    SIMILARITY: Belongs to the fibril-associated interrupted helices (FACIT) family. SIMILARITY: Contains 8 fibronectin type-III d SIMILARITY: Contains 1 TSP N-terminal (TSPN) SIMILARITY: Contains 2 VWFA domains.
                s Swiss-Prot entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION:
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ota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                Lysines at the third position of the tripeptide repeating (G-X-Y) are hydroxylated in all cases and bind carbohydrates Prolines at the third position of the tripeptide repeating (G-X-Y) are hydroxylated in some or all of the chains.
                                                                                                                                                                                                                                                                                                                                                        LLULAR LOCATION: Extracellular matrix.

3 SPECIFICITY: Wide tissue distribution; high presence connective tissue in skeletal muscle.
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E., Penin F., Deleage G., Dublet B.,
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RESULT COCA1_C

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lel. 13, lel. 35, lel. 47, lel. 47,

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Collagen alpha

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PDB; 189Q; NMR; A=1833-1885.
InterPro; IPRO08160; Collagen.
InterPro; IPRO03961; FN III.
InterPro; IPRO0395; VWF_A.
Pfam; PP01391; Collagen; 4.
Pfam; PP00041; fn3; 8.
Pfam; PF00092; VWA; 2.
PRINTS; PR00453; VWFADOMAIN.
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PROSITE; PS50234; VWFA; 2.
3D-structure; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X70793; CAA50064 1; -; EMBL; X70792; CAA50063 1; -; EMBL; X66138; CAA46928 2; -; EMBL; X65122; CAA46238 1; -;
                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .A45974; A45974.
S78476; S78476.
278
                 123
                                                                         158
                                                       63
                                                                                           ω
                                                                                                              61;
                                                                                                                        Similarity
                                                 GEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPVGP
                                                                         DIVILVOGSWSIGRFNFRLVRLFLENLVSAFNVGSEKTRVGLAQYSGDPRIEWHLNAYGT
                                                                                           DIMFLIDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS
                PMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGSI 178
                                    KDAVLDAVRNLPYKGGNTLTGLALTYILENSFKPEAGARPGVSKIGILITDGKSQDDVIP
PAKNIRDAGIELFAIGVKNADINĖLKEI ASEPDSTHVYNVADFNFMNSIVEGLTRTV
                                                                                                                                                                                                                                     1469
1664
1489
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1042
1239
1227
                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   Hydroxylation;
                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                   830
921
1009
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1468
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138
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1856
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117
330
440
532
621
711
                                                                                                                      29.1%;
                                                                                                                                                   202668 MW;
                                                                                                                                                                                                                       Triple-helical region (NC4).
Triple-helical region 1 (Ct.
Triple-helical region 2 (Cf.
Cell attachment sir-
Cell attachment sir-
                                                                                                              33;
                                                                                                            Score 265.5;
Pred. No. 2.9e
33; Mismatches
                                                                                                                                                                                                                                                                                            Fibronectin type-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA.
                                                                                                                                                                                                                                                                                                                                                                                          Repeat; Sig
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA.
                                                                                                                                                                                                                                                                                                                                                                       Fibronectin
                                                                                                                                                                                                                                                                                                                                                                                 Collagen alpha 1(XIV)
                                                                                                                                                                                                                                                                                                                                                                                                             Collagen;
                                                                                                                                                    39915BB9F46DD873
                                                                                                                                                                                                                             attachment site (Potential).
attachment site (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                   signal;
                                                                                                                                                                                                 (GlcNAc. . (GlcNAc. .
                                                                                                                                                                                                                                                                                                                                                                                                            Extracellular matrix;
                                                                                                                        .9e-14
                                                                                                                                                                                                                                                                                                                                                                        type-III
                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                    Structural
                                                                                                               82;
                                                                                                                                 Length
                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                               8 7 6 5 4 8 2
                                                                                                                Indels
                                                                                                                                                                                                                                       1 2 (COL1).
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                 chain.
                                                                                                                                                                                                  (Potential) (Potential)
                                                                                                                                                                                                                                                          (COL2)
                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                             1:
                                                                                                               Gaps
                                      277
                                                         122
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STRAIN-White leghorn;
STRAIN-White leghorn;
MEDLINE-92011862; PubMed=1918137; DOI=10.1083/jcb.115.1.209
Vamanara M., Yamada K.M., Yamada S.S., Shinomura T., Tanaka
                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95370352; PubMed=7642694; DOI=10.1083/jcb.130.4.1005; Koch M., Bohrmann B., Matthison M., Hagios C., Trueb B., Chiquet "Large and small splice variants of collagen XII: differential expression and ligand binding.";
                                                                                                                                                                                                                                                                                                                                                                                                                                       Trueb J., Trueb B.;
"The two splice variants of collagen XII share contain Biophys. Acta 1171:97-98(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete primary structure of type XII collagen shows a chimeric molecule with reiterated fibronectin type III motifs, von Willebrand factor A motifs, a domain homologous to a noncollagenous region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamagata M., Yamada K.M., Yamada Nishida Y., Obara M., Kimata K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=COL12A1;
Gallus gallus (Chic)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Type XII collagen. A large
             -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93042014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Type XII co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=87317590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90062079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                 Cell Biol. 130:1005-1014(1995).

FUNCTION: Type XII collagen interacts with type I collagen-
containing fibrils, the COL1 domain could be associated with the
surface of the fibrils, and the COL2 and NC3 domains may be
localized in the perifibrillar matrix.

SUBUNIT: Trimer of identical chains each containing 190 kDa of
nontriple-helical sequences.

ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell Biol. 115:209-221(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA
                                                                                                                                                              Event-Alternative splicing; Named isoforms=2; Comment=The final tissue form of collagen XII may contain homotrimers of either isoform Long or isoform Short or an combination of isoform Long and isoform Short. Only isofor is a proteoglycan. Isoform Long has more restricted expres in embryonic tissue than isoform Short;
             PTM:
                                    IsoId=P13944-2; Sequence=VSP_001148; TISSUE SPECIFICITY: Type XII collagen is pre ligaments, perichondrium, and periosteum, al tissues containing type I collagen.

DOMAIN: This sequence defines five distinct helical domains (COL1 and COL2) and three no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2846-2873
                          domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IX collagen, and short collagenous domains
.";
                                                                                                                                        IsoId=P13944-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cloning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IX collagen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            collagen: distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acad.
           (NC1, NC2, and NC3). triple-helical tail is
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cetazoa; Chordata; Craniata; Vertebrata; Buteleostomi;</pr>
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerecke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264:19772-19778(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=1420368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=3476925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=2584192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF 2960-3076.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D.R.,
                                                                                                                                       Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-1283 (ISOFORM SHORT), AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2456-3124,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olsen B.R.; ct extracellular matrix component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dublet B., va
e multidomain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84:6040-6044(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOI=10.1016/0167-4781(92)90145-P;
             stabilized
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molecule with
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dense
             disulfide bonds
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connective
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EMBL; D00824; BAA00701.1;
EMBL; X61024; CAA43358.1;
EMBL; M7375; AAA489718.1;
EMBL; J05137; AAA48655.1;
EMBL; X67327; CAA47744.1;
                                                                                                                                                CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00453; VWFADOMAIN.
SMART; SM00060; FN3; 18.
SMART; SM00210; TSPN; 11.
SMART; SM00327; VWA; 4.
PROSITE; P850853; FN3; 18.
PROSITE; P850853; FN3; 18.
PROSITE; P850234; VWFA; 4.
Alternative splicing; Cell adhesion; Collagen;
Direct protein sequencing; Extracellular matrix;
                                   REGION
REGION
                                                                                                            DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01391; Collagen; 4. Pfam; PF00041; fn3; 17. Pfam; PF00092; VWA; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                   DOMAIN
REGION
                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                  Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A40020; A40020.
                                                                         REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 18 fibronectin ty
SIMILARITY: Contains 1 TSP N-terminal
SIMILARITY: Contains 4 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIM:
PIM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (By similarity).
SIMILARITY: Belongs to the fibril-associated interrupted helices (FACIT) family.
SIMILARITY: Contains 18 fibronectin type-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P56199; 1QC5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           t (G-X-Y) are hydi
: O-glycosylated;
similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prolines at the third position of the tripeptide repeating (G-X-Y) are hydroxylated in some or all of the chains. O-glycosylated; glycosaminoglycan of chondroitin-sulfate t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENSGALG00000015908;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat; Signal; Structural protein.
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FN_III.
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Fibronectin type-III 1
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                                  imperfection.
Nonhelical region (NC2
Triple-helical region
                                                                     TSP N-terminal.
Nonhelical region (NC:
Triple-helical region
                                                                                                               VWFA
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Fibronectin
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                    imperfections.
                                                                                                                                                                                                                                                      VWFA
          Nonhelical
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         region
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type-III
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           (NC1)
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10
 (Potential)
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                                    (COL1)
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Best Local S
Matches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MATIN4 MOUSE STANUARY,
089029; O89030; Q9QWS3;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
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[2]
[2]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM DANS).
STRAIN=C57BL/6J; TISSUE=Mammary gland;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; DOI=10.1073/pnas.24260389;
MEDLINE=22388257; DOI=10.1073/pnas.24260389;
MEDLINE=22388257; DOI=10.1073/pnas.24260389;
MEDLINE=2288257; DOI=10.1073/pnas.24260389;
MEDLINE=2288257; DOI=10.1073/pnas.24260389;
MEDLINE=2288257; DOI=10.1073/pnas.242603899;
MEDLINE=2288257; DOI=10.1073/pnas.24287;
MEDLINE=2288257; DOI=10.1073/pnas.24287;
MEDLINE=2288257; DOI=10.1073/pnas.24287;
ME
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COMPBIAS
CARBOHYD
                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE (ISOFORMS LONG AND SHORT), AND VARIANTS.
STRAIN-C57BL/6J, and CD-1; TISSUB-Fetal;
MEDLINE=98442849; PubMed=9771906 DOI=10.1016/S0014-5793(98)01111-9;
Wagener R., Kobbe B., Paulsson M.;
"Matrilin-4, a new member of the matrilin family of extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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T -> S (in Ref. 4).
D -> E (in Ref. 2).
P -> A (in Ref. 2).
L -> F (in Ref. 2).
V -> F (in Ref. 2).
QP -> AG (in Ref. 3).
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Ra Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villahon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villahon D.K., Wolfey R., Sodergren E.J., Lu X., Gibbs R.A., Ra Fahey J., Helton B., Xetteman M., Madan A., Rodrigues S., Sanchez A., RA Fahey J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Bouterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences."
     Pfam; PF000008; EGF; 4.

Pfam; PF000092; VWA; 2.

PIRSF; PIRSF015217; Math VWA; 1.

PRINTS; PR00453; VWFADDMĀIN.

PROSITE; PS00010; ASX HYDROXYL; 2.

PROSITE; PS01186; EGF 2; 2.

PROSITE; PS50026; EGF 3; FALSE NEG.

PROSITE; PS50026; EGF 3; FALSE NEG.
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DOMAIN
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EMBL; AJ006140; CAA06890.1;
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EMBL; AJ010984; CAA09451.1;
HSSP; P00736; 1APQ.
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FEBS Lett. 438:165-170(1998).
-!- FUNCTION: Major component of the extracellular matrix
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GO; GO:0005615; C:extracellular space; TAS
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MEDLINE=99043241; PubMed=9827539;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isoid=089029-2; Sequence=VSP_001401;
TISSUE SPECIFICITY: Lung, brain, sternum, kidney and heart.
DEVELOPMENTAL STAGE: The short isoform was detected in 7 we mice but not in developing mice (19.5 dpc embryos or in 2, 21 days old animals).
SIMILARITY: Contains 4 EGF-like domains.
SIMILARITY: Contains 2 VWFA domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
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0; IPR00742; EGF_2.
0; IPR06209; EGF like.
0; IPR011203; Matn_vWA.
0; IPR012035; VWF_A.
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splicing; Coiled coil; EGF-like
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Potential.
22 624 Matrilin-4.
36 215 VWFA 1.
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13-SEP-2005
13-SEP-2005
Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Luffalla G., Dossat C., Segurens Nicaud S., Jaffe D., Fisher S., Luffalla G., Dossat C., Segurens Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V. Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
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63 TETNG
Q4SH63_1
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COILED
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CARBOHYD
DISULFID
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Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metozoa; Chordata; Teleostei; Euteleostei; Neoteleostei;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequ
13-SEP-2005 (TrEMBLrel. 31, Last anno
Chromosome 8 SCAF14587, whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
VARIANT
                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                         Tetradontoidea; T
NCBI_TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAEVAAQARARGIEIYAVGVQRADVGSLRTMASPPLDQHVFLVESFDL---IQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REDMERATRAVVPLAQGTMTGLATQYAMNVAFSEAEGARPSEERVPRVLVIVTDGRPQDR
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By similarity

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By similarity.

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By similarity.

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By similarity.

338

By similarity.

340

By similarity.

351

By similarity.

9

Missing (in isoform Short).

/FTIG-VSP 001401.

A -> E (in strain C57BL/6J).

DFA28D2C94B1A14F CRC64;

"e 265; DB 1; Lenr"

No. 9.2e-15;
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Last annotation update)
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                                                 Robinson-Rechavi
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                                                                                        Bosak
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Best Local S
Matches 61
[3]
NUCLEOTIDE SEC...
Coxby N.;
Coxby N.;
Submitted (MAY-2005) to the EM
Submit AL354664; CAH71309.1; -/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K2 HUMAN
Q5VYK2 HUMAN
Q5VYK2;
                                                                                                                                                                                                                                                                                    Tromans A
Submitted
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NON TER
SEQUENCE
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[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collagen, type XII, alpha 1.
Name=COL12A1; ORFNAmes=RP1-238D15.1-003;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-2005 (TrEMBLrel. 29,
01-FEB-2005 (TrEMBLrel. 29,
13-SEP-2005 (TrEMBLrel. 31,
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SMART; SM00060; FN3; 6.
SMART; SM00210; TSPN; 1.
SMART; SM00327; VWA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01391; Collagen; Pfam; PF00041; fn3; 6. Pfam; PF00092; VWA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope; Whitehead Institute (
Submitted (FEB-2004) to the EMBI
-!- CAUTION: The sequence shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50853; FN3; 7.
PROSITE; PS50234; VWFA; 2.
Collagen; Extracellular matrix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary data.
EMBL; CAAE01014587; CAG00019.1;
InterPro; IPR008160; Collagen.
InterPro; IPR003961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype.";
                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003129; Laminin_G_TSP_N.
InterPro; IPR002035; WF_A.
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                                                                                                                                                                                                                                                                                                                                                                                   [_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNKVSKEMOMDGYIIFAIGFADADYGELVNIASKPSDRHVFFVDDLDAVKKIEEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSNKEALLEAIQKISYKGGNTKTGRAIKHVKESIFSLEAGARRGVPKVLVVLTDGRSQDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDP
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                                                                                                                                                                                     (MAY-2005)
                                                                                                                                                                                                                                                                                       (MAY-2005)
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nilarity 34.7%;
Conservative 38
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                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
                          EMBL/GenBank/DDBJ
-; Genomic_DNA.
-; Genomic_DNA.
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Last
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                                                                                                                                                                                     EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 265; DB 2;
Pred. No. 2.6e-14;
8; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence up
annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6203E9A0900C6D9D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75;
                                                                                                                                                                                     databases
                                                                                                                                                                                                                                                                                       databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
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88888

Ensembl;

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localized in the perifibrilla SUBUNI: Trimer of identical nontriple-helical sequences. ALTERNATIVE PRODUCTS:

of the

fibrils,

ibrils, and the COL2 and NC3 domains perifibrillar matrix (By similarity) of identical chains each containing 1

domains may

ьe

190 kDa

Off.

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R InterPro; IPRO03961; FN III.

R InterPro; IPRO03961; FN III.

R InterPro; IPRO0303129; Laminin_G_TSP_N.

R InterPro; IPR002035; VWF_A.

R InterPro; IPR002035; VWF_A.

R Pfam; PF00391; Collagen; 2.

R Pfam; PF004041; fn3; 18.

R Pfam; PF00092; VWA; 4.

R Pfam; PF00093; VWFADOMAIN.

R SMART; SM000160; FN3; 18.

RR SMART; SM000160; TSPN; 1.

RR SMART; SM000327; VWA; 4.

RR SMART; SM00327; VWA; 4.

RR SMART; SM00327; VWA; 4.

RR SMART; SM00327; VWA; 4.

RR PROSITE; PS503234; VWFA; 4.

RR PROSITE; PS503234; VWFA; 4.

COllagen; Extracellular matrix; Repeat; Structural protein.

SEQUENCE 2884 AA; 315869 MW; 2D598F13656E454D CRC64;
collagen (vuzzza) collagen (vuzzza) (enromosome 6q12-q13."; Chromosome 6q12-q13."; Genomics 41:236-242(1997) (enromics 41:242(1997) (e
                                                                                                                                  Gerecke D.R., Olson P.F., Koch M., Knoll J.H.M., Taylor R., Hudson D.L., Champliaud M.-F., Olsen B.R., Burgeson R.E.; "Complete primary structure of two splice variants of collagen and assignment of alpha I(XII) collagen (COL12A1), alpha I(IX) collagen (COL19A1), and alpha 1(XIX) collagen (COL19A1) to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GOCAL HUMAN STANDARD; PRT; 3063 AA. Q99715; Q99716; 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Collagen alpha 1(XII) chain precursor.
Name=COL12A1;
                                                                                                                                                                                                                                                     SEQUENCE.
MEDLINE=97288521; PubMed=9143499; DOI=10.1006/geno.1997.4638;
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GO:0005578; C:extracellular matrix (sensu Metazoa);
GO:0005198; F:structural molecule activity; IEA.
GO:0007155; P:cell adhesion; IEA.
GO:0006817; P:phosphate transport; IEA.
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AL080250; CAH71309.1; JOINED; Genomic DNA.
AL096771; CAH71309.1; JOINED; Genomic DNA.
AL354664; CAI19897.1; JOINED; Genomic DNA.
AL080250; CAI19907.1; JOINED; Genomic DNA.
AL354664; CAI19907.1; JOINED; Genomic DNA.
AL096771; CAI1997.1; JOINED; Genomic DNA.
AL096771; CAI1997.1; JOINED; Genomic DNA.
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                                                                                                                                                                                                                                                                                                             (ISOFORMS LONG AND SHORT), AND PARTIAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Hominidae;
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No. 7.2e-14;
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                                             InterPro; IPR008160; Collagen.
InterPro; IPR003961; FN III.
InterPro; IPR002035; VWF A.
Pfam; PF01391; Collagen; 4.
Pfam; PF00041; fn3; 18.
Pfam; PF00092; VWA; 4.
                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U73778; AAC51
EMBL; U73779; AAD40
HSSP; P18614; 1MHP.
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                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                Alternative splicing; Cell adhesion; Collagen; Direct protein sequencing; Extracellular matrix;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
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GO; GO:0001501; P:skeletal development; TAS
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SIMILARITY: Belongs to the fibril-associated collagen interrupted helices (FACIT) family.
SIMILARITY: Contains 18 fibronectin type-III domains.
SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
SIMILARITY: Contains 4 VWFA domains.
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PTM: Prolines at the third position of the tripeptide unit (G-X-Y) are hydroxylated in some or all of the cl
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PTM: O-glycosylation of isoform Long; glycosaminoglycan
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TISSUE SPECIFICITY: Found in collagen I-containing tissues isoform Short and isoform Long appear in amnion, chorion, muscle, small intestine, and in cell culture of dermal fibroblasts, keratinocytes and endothelial cells. Only the isoform is found in lung, placenta, kidney and a squamous carcinoma cell inco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Short;
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Comment=The final tissue form of collagen XII
homotrimers of either isoform Long or isoform
combination of isoform Long and isoform Short;
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O-linked (Xyl...) (chondroi (Potential).
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Pred. No. 7.7e-14;
0; Mismatches 84;
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Nonhelical region (NC2).
Triple-helical region (COL1) with
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14 droxyproline (By similarity).
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Result
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-MODEL-frame+ n2p.model -DEV=xlp
-Q-|abss/ABSSWEB spool/US10699035/runat_13022006_062440_25403/app_query.fasta_1
-Q-|abss/ABSSWEB spool/US10699035/runat_13022006_062440_25403/app_query.fasta_1
-DB=A Geneseq -QFMT-fastan -SUPFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALICM=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALICN=15 -MODEL-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10699035 @CGN 1 1 476 @runat 13022006_062440_25403 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -WAIT -DSPBLOCK=100 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum Match 100%
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seq length: 2000000000
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Ygapop 10.0 , X
Fgapop 6.0 , I
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ALIGNMENTS

RESULT 1 AAE32502 Disulfide-bond Willebrand Factor A domain related-protein; von Willebrand Factor A; VA; extracellular matrix; ECM; molecular marker; cartilage; arthritis; WARP; Misc-difference Key Homo sapiens. gene therapy; Human Willebrand Factor A domain related-protein (WARP). 24-MAR-2003 (first entry) AAE32502; AAE32502 standard; protein; 418 Modified-site Modified-site Modified-site Modified-site Protein Peptide human. 369. /note= "O-glycosylation site"
210. .211 /note= "N-glycosylation site"
361 359 148 Location/Qualifiers /note= "N-glycosylation site" /note= note= "0-glycosylation site" label= Signal_peptide note= . 393 "Encoded by CTCGCG" "Human mature WARP protein" A

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                                         AAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCAGGGGTGCCCAAAGTGCTGGTG
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ABP69674 protein; 445

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ABP69674;

20-JAN-2003 (first

Human polypeptide SEQ ID NO 1721.

entry)

Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; fungicide; protozoacide;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or p
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                                                                   AGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTTCGGGAGTTTGTGGGGGAGCTG
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          ValAlaProLeuProLeuGlyThrGlyAlaLeuArgAlaSerLeuValHisValGlySer
                           GTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGTGCCAGTCTGGTGCACGTGGGCAGT
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Wang D, Drmanac RT;
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2002US-038694P
2002US-0386971P
2002US-0386971P
2002US-0387626P
2002US-0387610P
2002US-0387610P
2002US-0387610P
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2002US-0387696P
2002US-0387696P
2002US-0387696P
2002US-0387696P
2002US-0387934P
2002US-0387934P
2002US-0387934P
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2002US-0399006P
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2002US-0401528P
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12-AUG-2002

12-AUG-2002

12-AUG-2002

13-AUG-2002

13-AUG-2002

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13-AUG-2002

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13-AUG-2002

13-AUG-2002

13-AUG-2002

26-AUG-2002

26-AUG-2002

27-AUG-2002

28-CCT-2002

30-SEP-2002

30-SEP-2002

30-SEP-2002

31-GCT-2002

31-GCT-2002

28-CCT-2002

21-GUT-2002

21-GUT-2002
                                                                                    The invention relates to a novel isolated polypeptide (NOVX). A polypeptide of the invention has cytostatic, immunomodulator, neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and antilipaemic activity, and may have a use in gene therapy, and as a vaccine. The polypeptides are encoded by NOVX polynucleotides comprising any of the 303 fully defined nucleotide sequences given in the specification. The polypeptide is useful in the manufacture of a medicament for treating a syndrome associated with a human disease. The polypeptide, polynucleotide and antibody are useful in diagnosing, treating or preventing NOVX-associated disorders, e.g. cancer, cachexia, Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious disease, metabolic syndrome X or dyslipidaemias. The nucleic acids are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ; Catterton E, Chapoval A, Crabbree-Bokor JR, Edinger SR, Ellerman Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall Mclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS; Paddigaru M, Patturajan M, Pezkick AJ, Millet I, Rastelli Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA; Smithbon G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                    New NOVX polypeptides and nucleic acid molecules useful for preventing treating NOVX-associated disorders, e.g. cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
                                represents a NOVX polypeptid
                                  further used as hybridisation probes, in chromosome typing, preventive medicine, and pharmacogenomics. 'represents a NOVX polypeptide of the invention.
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2002US-0403517P.
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2002US-0410840P.
2002US-04112528P.
2002US-04112528P.
2002US-04112538P.
2002US-04114839P.
2002US-04114840P.
2002US-04114840P.
2002US-0417186P.
2002US-042063P.
2002US-0421156P.
2002US-0421156P.
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Length: Matches:

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                                                                                                         GlyTyrTyrValLeuGluLeuValProSerAlaGlnProGlyAlaAlaArgArgGlnGln
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WPI; 2003-111873/10.
N-PSDB; AAD50022, AAD50398
                                               Bateman JF,
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Mouse Willebrand Factor A (first entry) domain related-protein (WARP).

Willebrand Factor A domain related-protein; von Willebrand Factor A; VA; extracellular matrix; ECM; molecular marker; cartilage; arthritis; WARP; gene therapy; mouse.

1. 18 /label= Signal_peptide 19. .415 Location/Qualifiers

/note= "0-glycosylation 369..393 /note= "N-glycosylation 359 264 148 note= note= note= "N-glycosylation "O-glycosylation site" "Mouse mature WARP protein" site" site" site"

note= "0-glycosylation"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kidney injury-associated molecule, KIM, injured or regenerating tissues, useful regeneration, especially to treat renal
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CC which encode human secretory or membrane proteins represented by AAB8817
CC - AAB88419. Included in the invention are primers AAF93917
CC - AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the CC invention. The invention also includes methods for the production of the cantibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polymucleotide sequences can be used in gene CC therapy. The polymucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated CC with inappropriate secretory protein/membrane protein expression. The CC nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. CC proteins/membrane polypeptides and their role in metabolism. The CC polypeptides may be used as antigens in the production of secretory proteins/membrane polypeptides and their role in metabolism. The CC antagonists had in assays to identify modulators (agonists and CC antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be the presence of the polypeptides in samples (e.g. by enzyme CC treated inmunosorbant assay (EJISA). Examples of diseases which may be treated include rheumatoid arthritis and diabetes
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   membrane proteins, and their coding sequences. The present sequence is one such protein sequence. The coding sequences of the invention are useful for examination and diagnosis of abnormality of the human secretary proteins and in gene therapy methods. The coding sequences and proteins are useful as candidates for medicines or as target molecules for developing medicines. Antibodies against the proteins of the invention are useful for treating diseases that are associated with the proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained from sequence information supplied by the European Patent Office.
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                                                                                                                                                                                  Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                     Claim
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;

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AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87342-AAB87413 represent the proteins they encode. AAB87414-AAB87454 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ni J, Baker KP,
Soppet DR, Young
Moore PA, Shi Y,
                                                                                                                                                                                                                                                                                                                                                                   preventing, treating Parkinson's diseases
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                                                                         GCTGCCTCAGCCCCTGCCGAGAAGCACCTGCACTTTGTGGACGTGGATGACCTGCACATC
                                                                                                                             TrpValThrAspGlyGlySerSerAspProValGlyProProMetGlnGluLeuLysAsp
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Query Match:
US-10-699-035A-5 (1-1254) x ABG65347 (1-215)
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                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The protein X are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutsfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
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                            12-APR-2000; 2000US-0229358P
25-APR-2000; 2000US-0199384P
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(ROSE/) ROSEN C A. (HASE/) HASELTINE
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New albumin fusion proteins, useful for diagnosing, treating, or ameliorating diseases or disorders e.g. cancer, anemia, ariasthma, inflammatory bowel disease or Alzheimer's disease. , treating, preventing anemia, arthritis,

Disclosure; SEQ ID NO 2096; 279pp; English

Cdisorder in a patient computa; a method of treating a cisease or cdisorder in a patient computating the step of administering the albumin CC fusion protein; a method of treating a patient with a disease or disorder that is modulated by Therapeutic protein: X, or its fragment or variant; CC a method of extending the shelf life of Therapeutic protein: X, or its fragment or variant; a nucleic acid molecule comprising a polynucleotide sequence encoding the albumin fusion protein; a vector comprising the comprising the encleic acid molecule of the albumin fusion protein; and a host cell comprising the nucleic acid molecule of the albumin fusion protein. The activities: cytostatic, antianemic, antiarchritic, antiasthmatic, antiacterial, osteopathic, dermatological, antigout, immunomodulator, antiarrhythmic, cardiant, nootropic, antilipaemic, nephrotropic, uropathic, neuroprotective, antiparkinsonian, tranquilizer, antidiabetic, anabolic, hypertensive, and vulnerary. The albumin fusion protein nucleic acid may be used in gene therapy to treat disorders. The albumin fusion protein is cancer (e.g. leukaemia, colon, bone, breast, liver or lung cancer), cancer (e.g. leukaemia, colon, bone, breast, liver or lung cancer), cancer (e.g. leukaemia, colon, bone, breast, liver or lung cancer), cancer (e.g. neamnia, multiple myeloma, arthritis, asthma, ALDS, autoimmune disease, inflammatory bowel disease, psoriasis or Lyme (e.g. disease), reproductive system disorders (e.g. prostatitis, inguinal carcinoma, variacocela, penile carcinoma, ovarian adenocarcinoma or Sertoli-levidiseases), musculoskeletal diseases (e.g. rhabdomyomas, heart disease, acute carchexia), cardiovascular diseases (e.g. rhabdomyomas, heart disease, acute carchythmia, cardiovascular diseases (e.g. rhabdomyomas, heart disease, or Tay or syndrome, batal syndrome. Turner's syndrome, bart syndrome, or Tay CC Down's syndrome, Patau Syndrome, Turner's syndrome, Apert syndrome or Tay (CC -Sachs disease), excretory diseases (e.g. urinary incontinence, urinary (cc tract infections or renal disorders), neural or sensory disease (e.g. CC Alzheimer's disease, Parkinson's disease, cerebral malaria, meningitis, (cc cerebellar ataxia, attention deficit disorder, autism or obsessive (cc computsive disorder), respiratory disease (e.g. emphysema, lung cancer or (cc contextional lung disease), endocrine disease (e.g. diabetes, Addison's disease or glomerulonephritis), digestive diseases (e.g. portal (competitive tissue or epithelial disease) (e.g. Crohn's disease, and or connective tissue or epithelial disease (e.g. Crohn's disease, corporate a therapeutic protein x relating to the albumin fusion protein (corporation). This sequence corporation in the invention. The sequence listing data for this specification was completed from the USPTO website. further relates to: a composition comprising the albumin fusion pand a pharmaceutical carrier; a kit comprising the composition of albumin fusion protein formula; a method of treating a disease or relates to a novel albumin fusion protein. of the

Sequence

Best Local S Query Match: Percent Similarity: Best Local Similarity: Score: 5.95e-65 1067.50 99.1% 99.1% 44.9% Mismatches: Indels: Gaps: Matches: Conservative:

US-10-699-035A-5 (1-1254) x ADL78614 (1-215)

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                                                                                                                               foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alcheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; cell culture; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification.
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                                                                                                                                                                                                                                                                                                                                                                                         standard;
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MetLeuProTrpThrAla***GlyLeuAlaLeuSerLeuArgLeuAlaLeuAlaArgSer GGCGCGGAGCGCTCCACCAGCATCAGCCCCCCGAGGGGACCTGATGTTCCTGCTGGAC

ATGCTCCCCTGGACGGCCTCGGCCCTGAGCTTGCGGCTGGCGCTGGCGCGGAGC

US-10-699-035A-5 (1-1254) x AAB87418

(1-242)

Gaps: Mismatches: Indels:

Best Local S Query Match:

Similarity:

6.09e-65 1067.50 199.1% 99.1% 44.9%

Length:
Matches:
Conservative:

Score: Alignment

No.:

Percent Similarity:

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121 83

48 61 28

181

GTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCGTGCCAGTCTGGTGCACGTGGGCAGT

240 87 180 67 120 47 60

SerSerAlaSerValSerHisTyrGluPheSerArgValArgGluPheValGlyGlnLeu AGCTCAGCCAGCGTCTCTCACTACGAGTTCTCCCGGGTTCGGGGAGTTTGTGGGGCAGCTG GlyAlaGluArgGlyProProAlaSerAlaProArgGlyAspLeuMetPheLeuLeuAsp

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CC AIDS, autoimmane diseases (e.g., rheumatoid arthritis), inflammation, callergies, neurological disorders (e.g., Alzheimer's disease, reurological disorders (e.g., Alzheimer's disease, atheroscierosis, cardiovascular disorders, sepsis, diabetes, atherosclerosis, cardiovascular disorders, sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine consistent and infections. The proteins can also be used to aid wound the self-gradient organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

CC antibodies specific for a protein of the invention can be used in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human can be carried to in the disorders mention as an entire the invention can be used in the corrected protein fragment referred to in the disclosure of the invention can be used in the corrected protein fragment referred to in the disclosure of the invention can be used in the corrected protein fragment referred to in the disclosure of the invention can be used in the corrected protein fragment referred to in the disclosure of the invention can be used in the corrected protein fragment referred to in the disclosure of the invention can be used in the corrected protein fragment referred to in the disclosure of the invention can be used in the corrected protein fragment referred to in the disclosure of the invention can be used in the corrected protein fragment referred to in the disclosure of the invention can be used to an entire the corrected protein fragment referred to in the disclosure of the invention can be used to an entire the corrected protein fragment 
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Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers.
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Disclosure; Page 18; 607pp; English

cc and their corresponding secreted proteins are useful for preventing, cc treating or ameliorating medical conditions, e.g., by protein or gene clearing or ameliorating medical conditions, e.g., by protein or gene conterapy. Pathological conditions can be diagnosed by determining the amount of the new genes. Specific uses are described for each of the camount of the new genes. Specific uses are described for each of the candinal include developing products for the diagnosis or treatment of candinal include developing products for the diagnosis or treatment of candinal include developing products for the diagnosis or treatment of the conditions autoimmune diseases (e.g., reumatoid arthritis), inflammation, cc AIDS, autoimmune diseases (e.g., reumatoid arthritis), inflammation, cc disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cc ardiovascular disorders, angiogenic disorders, stinzophrenia, asthma, skin cc disorders, and infections. The proteins can also be used to aid wound ce disorders, and infections. The proteins can also be used to aid wound condition or paint before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used can a food additive or preservative to modify storage properties.

Cc Antibodies specific for a protein of the invention can be used in diagnostic immunoassays (ELISA). The present sequence represents a human cc ancreted protein fragment referred to in the disclosure of the invention cc secreted protein fragment referred to in the disclosure of the invention cc secreted protein fragment referred to in the disclosure of the invention cc. AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87342-AAB87413 represent the proteins they encode. AAB87414-AAB87454 represent human secreted protein fragments. The genes

Alignment Pred. No.: US-10-699-035A-5 (1-1254) x AAB87424 Best Local Percent Similarity: Similarity: 1.44e-64 1062.00 100.0% 100.0% 44.6% (1-226)Length: Matches: Conservative: Gaps: Mismatches: Indels: 226 210 0 0

Sequence

Ş Ś 문 S 밁 Ş B Ş 밁 Ş 뮍 Ş 361 301 114 241 181 121 74 54 34 61 14 94 GTGCGTGCTTCTGCCCAGCGCATGGGTGACACCCACACTGGCCTGGCCTGGTCTATGCC ValAlaProLeuProLeuGlyThrGlyAlaLeuArgAlaSerLeuValHisValGlySer GlyAlaGluArgGlyProProAlaSerAlaProArgGlyAspLeuMetPheLeuLeuAsp GECGCGGAGCGCCGCCAGCATCAGCCCCCCGAGGGGACCTGATGTTCCTGCTGGAC AAGGAACAGCTGTTTGCTGAAGCATCAGGTGCCCGGCCAGGGGTGCCCAAAGTGCTGGTG CGGCCATACACCGAGTTCCCCCTTCGGCCAGCACAGCTCGGGTGAGGCTGCCCAGGATGCG GTGGCTCCACTGCCCCTGGGCACCGGGGCCCTGCCTGCCAGTCTGGTGCACGTGGGCAGT SerSerAlaSerValSerHisTyrGluPheSerArgValArgGluPheValGlyGlnLeu AGCTCAGCCAGCGTCTCCACTACGAGTTCTCCCGGGTTCGGGGAGTTTGTGGGGGCAGCTG MetLeuProTrpThrAlaLeuGlyLeuAlaLeuSerLeuArgLeuAlaLeuAlaArgSer ATGCTCCCTGGACGGCGCCGGCCTGGCCCTGAGCTTGCGGCTGGCGCTGGCGCGGAGC ValArgAlaSerAlaGlnArgMetGlyAspThrHisThrGlyLeuAlaLeuValTyrAla 53 υ u 153 420 133 360 113 300 73 180 120 93 240

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                    AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87342-AAB87413 represent the proteins they encode. AAB87414-AAB87454 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the represence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of
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RESULT 15
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Human von Willebrand Factor A (VA) domain.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC abnormalities, haematopoietic disorders, diseases of the immune system, CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, CC allergies, neurological disorders (e.g., Alzheimer's disease, CC altergies, neurological disorders (e.g., Alzheimer's disease, CC Parkinsons's disease), cognitive disorders, schizophrenia, asthma, skin CC cardiovascular disorders, sepsis, diabetes, atherosclerosis, CC cardiovascular disorders, angiogenic disorders, kidney disorders, CC gastrointestinal disorders, pregnancy-related disorders, andocrine CC disorders, and infections. The proteins can also be used to aid wound CC suburn, to maintain organs before transplantation, for supporting cell CC culture of primary tissues, to regenerate tissues, to identify their CC cognate ligands or binding partners, and in chemotaxis, and can be used CC as a food additive or preservative to modify storage properties.

CC Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and con the invention seasy or enzyme linked and contains and can be used and contains or immunoassave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a huma secreted protein fragment referred to in the disclosure of the invo
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ProAlaProAlaAlaSerSerGlyProGlyArg***ProSerArgGlyAla
                                                                          GlyThrSerGlyProLeuGlyGlyLeuMetLeuValAspArgAlaProArgArgSerAla
                                                                                              GGAACATCAGGTCCCCTCGGGGGGGCTGATGCTGGTGGACCGCCGCTCCGCGCTCCGCG
                                                                                                                                               ProGlnThrProGluProGlyArgThrArgSerGluArgArgTrpLeuSerCysProAla
                                                                                                                                                                         ArgAlaProAspTrpHisAlaGlyProArgCysProGlyAlaValGluProProAlaAla
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                                     CCAGCGCCAGCCGCAAGCTCAGGGCCAGGCCGAGCGCCGTCCAGGGGAGCA
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                                                                                                                                                                                                                                                                           Score:
                                                                                                                                                                                                                                                                                                                                                           The invention relates to Willebrand Factor A domain related protein (WARP) which is a member of von Willebrand Factor A (VA) domain protein superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The
                                                                                                                                                                                                                                                                                                                          Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                present sequence is human VA domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 72-73; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bateman JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-2001; 2001AU-00004701
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                                                                                                                                                                                                                                                                                        No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        w isolated Willebrand Factor A-Related Protein polypeptide useful for
e manufacture of a medicament in the treatment of a disease condition
the extracellular matrix, in particular arthritis.
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                                                                                  GlyProProMetGlnGluLeuLysAspLeuGlyValThrValPheIleValSerThrGly
PheValAspValAspAspLeuHisIleIleValGinGluLeuArgGlySerIleLeu
            TTTGTGGACGTGGATGACCTGCACATCATTGTCCAAGAGCTGAGGGGCTCCATTCTC
                                          ArgGlyAsnPheLeuGluLeuSerAlaAlaAlaSerAlaProAlaGluLysHisLeuHis
                                                                                                GGCCCCCCATGCAGGAGCTCAAGGACCTGGGCGTCACCGTGTTCATTGTCAGCACCGGC
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Search completed: February 13, 2006, 13:23:41 Job time: 228.052 secs

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Result
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-DB=Published_Applications_AA_Main_-QFMT=fasta_n_-SUFFIX=rapbm_-MIMMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits_-START=1 -END=-1 -MATRIX=blosum62
-TRANKS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct_-THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto_-NORM=ext_-HEAPSTZE=500 -MINLEN=0
-MAXIEN=200000000 -HOST=abss02p
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-NO_MMAP_-NEG_SCORES=0_-WAIT_-DSPBLOCK=100_-LONGLOG_-DEV_TIMEOUT=120
-WARN_TIMEOUT=30_-THREADS=1_-XGAPOP=10_-XGAPEXT=0.5_-FGAPOP=6_-FGAPEXT=7
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Ygapop 10.0 , X
Fgapop 6.0 , E
Delop 6.0 , E
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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Sequence 20, Application US/10699035A
| Publication No. US20040214349A1
| GENERAL INFORMATION: Harman, John APPLICANT: Bateman, John APPLICANT: Fitzgerald, David TILE OF INVENTION: A Molecular Marker FILE REFERENCE: A36056 PCT USA A 071838.0142 CURRENT APPLICATION NUMBER: US/10/699,035A CURRENT FILING DATE: 2003-10-31 PRIOR APPLICATION NUMBER: PCT/AUU2/00542 PRIOR FILING DATE: 2002-05-02 PRIOR PILING DATE: 2001-05-02 PRIOR FILING DATE: 2001-05-02 NUMBER OF SEQ ID NOS: 40
| SOFTWARE: FASTSEQ for Windows Version 4.0 SEQ ID NO 20 LENGTH: 418 TYPE: PRT
| ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Bateman, John
APPLICANT: Bateman, John
APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838 0142
CURRENT FILING DATE: 2003-10-31
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2002-05-02
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 4
LENGTH: 415
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Bateman, John
APPLICANT: Bateman, John
APPLICANT: Bitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A35056 PCT USA A 071838 0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR FILING DATE: 2002-05-02
PRIOR PILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 415
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DB:
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; Publication No. US20040214349A1
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; ORGANISM: Homo sapiens ; PEATURE; ; NAME/KEY: SITE ; LOCATION: (7) ; OTHER INFORMATION: Xaa e US-09-789-561-85
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; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/24008
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,317
; PRIOR APPLICATION NUMBER: 60/152,315
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
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TITLE OF INVENTION: 52
FILE REFERENCE: PZ043P1
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; ORGANISM: Homo sapie
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SOFTWARE: Pacer
; SEQ ID NO 2096
; SEQTH: 215
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CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
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APPLICANT: Ni et al.

APPLICANT: Ni et al.

TITE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: PZ043P1

CURRENT APPLICATION NUMBER: US/10/883,936

CURRENT FILING DATE: 2004-07-06

PRIOR APPLICATION NUMBER: US/09/789,561

PRIOR FILING DATE: 2001-02-22

PRIOR PRIOR APPLICATION NUMBER: PCT/US00/24008

PRIOR FILING DATE: 2000-08-31

PRIOR APPLICATION NUMBER: 60/152,317

PRIOR APPLICATION NUMBER: 60/152,317

PRIOR APPLICATION NUMBER: 60/152,315

PRIOR APPLICATION NUMBER: 60/152,315

PRIOR APPLICATION NUMBER: 60/152,315

PRIOR APPLICATION NUMBER: 60/152,315

PRIOR FILING DATE: 1999-09-03

NUMBER OF SEQ ID NOS: 194
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DB:
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Best Local Similarity:
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SEQ ID NO 85
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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                                                            ValAlaProLeuProLeuGlyThrGlyAlaLeuArgAlaSerLeuValHisValGlySer
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Query Match:
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SEQ ID NO 159
LENGTH: 242
TYPE: PRT
ORGANISM: Homo s
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APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
NUMBER OF SEQ ID NOS: 194
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CURRENT FILING DATE: 2001-02-22
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NAME/KEY: SITE
LOCATION: (2)
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OTHER INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/883,936
CURRENT FILLING DATE: 2004-07-06
PRIOR APPLICATION NUMBER: US/09/789,561
PRIOR APPLICATION NUMBER: US/09/789,561
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
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SEQ ID NO 159
LENGTH: 242
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Publication No. US20050019866A1
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TITLE OF INVENTION: 52 Human secreted proteins
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                                                                                                                                                        LENGTH: 24
TYPE: PRT
                                                                                               NAME/KEY: SITE LOCATION: (2)
                             LOCATION: (5)
OTHER INFORMATION:
                                                                                    LOCATION: (2)
OTHER INFORMATION:
                                                                                                                                            ORGANISM: Homo
                                           NAME/KEY: SITE LOCATION: (5)
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TITLE OF INVENTION: 52 Human secreted protes in the reference: P2043P1 CURRENT APPLICATION NUMBER: US/09/789,561 CURRENT FILLING DATE: 2001-02-22 PRIOR APPLICATION NUMBER: PCT/US00/24008 PRIOR FILING DATE: 2000-08-31 PRIOR APPLICATION NUMBER: 60/152,317 PRIOR APPLICATION NUMBER: 60/152,315 PRIOR APPLICATION NUMBER: 60/152,315
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                                                                                                                                         Sequence 165, Application US/09789561
Patent No. US20020064818A1
GENERAL INFORMATION:
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Percent Similarity:
Best Local Similarity:
Query Match:
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; OTHER INFORMATION:
US-10-883-936-159
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Human secreted proteins

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; PRIOR FILING DATE: 19; NUMBER OF SEQ ID NOS: SOFTWARE: PatentIn Ve; SEQ ID NO 165; LENGTH: 226; TYPE: PRT; ORGANISM: Homo sapien US-09-789-561-165
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Sequence 165, Application US/10883936
Publication No. US20050019866A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted prot
FILE REFERENCE: PZ043P1
CURRENT APPLICATION NUMBER: US/10/883,936
CURRENT FILING DATE: 2004-07-06
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; PRIOR FILLING DATE: 2001-02-22
; PRIOR APPLICATION UNMBER: PCT/US00/24008
; PRIOR FILLING DATE: 2000-08-31
; PRIOR APPLICATION UNMBER: 60/152,317
PRIOR FILLING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILLING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 165
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-883-936-165
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600 193 540 173 480 153 420 133 360 113 300 93 240 73 180 53

Patent No. US20020064818A1

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CURRENT APPLICATION NUMBER: US/09/789,561
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 160
SEQ ID NO 160
LENGTH: 186
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Query Match:
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NAME/KEY: SITE
LOCATION: (152)
OTHER INFORMATION: )
NAME/KEY: SITE
LOCATION: (152)
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NAME/KEY: SITE
LOCATION: (184)
OTHER INFORMATION: Xaa
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ORGANISM: Homo sapiens
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                                                            GGAACATCAGGTCCCCTCGGGGGGCTGATGCTGGTGGACCGCGCTCCGCGCTCCGCG
                                                                                            ProGlnThrProGluProGlyArgThrArgSerGluArgArgTrpLeuSerCysProAla
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CURRENT FILING DATE: 2004-07-06
PRIOR APPLICATION NUMBER: US/09/789,561
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
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Publication No.
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LOCATION: (186)
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OTHER INFORMATION:
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
FILE REFERENCE: A36056 PCT USA A 071838.0142
FURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR FILING DATE: 2002-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-699-035A-2
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Publication No. US20040214349A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
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TYPE: PRT
ORGANISM: Homo
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                                                                                                   HisThrGlyLeuAlaLeuValTyrAlaLysGluGlnLeuPheAlaGluAlaSerGlyAla
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APPLICANT: YUE, Henry
APPLICANT: AZMEZAI, Yalda
APPLICANT: TANG, Y. Tom
APPLICANT: PATTERSON, Cha
APPLICANT: BAUGHN, Mariah
APPLICANT: LU, Dyung Aina
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CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/172,852; 60/172,354
PRIOR FILING DATE: 1999-12-10; 1999-12-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL Program
SEQ ID NO 18
LENGTH: 185
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Publication No. US20030044913A1
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ORGANISM: Homo &
FEATURE:
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APPLICANT: LAL, Preeti
APPLICANT: AU-YOUNG, Janice
APPLICANT: BURFORD, Neil
TITLE OF INVENTION: EXTRACELLULAR MATRIX AND
FILE REFERENCE: PF-0760 PCT
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Search completed: February 13, 2006, 13:53:31 Job time: 212.799 secs

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Copyright (c) 1993 - 2006 Biocceleration Ltd
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Willebrand Factor A domain related-protein; von Willebrand Factor A; VA; extracellular matrix; ECM; molecular marker; cartilage; arthritis; WARP; gene therapy; human.

Human von Willebrand Factor A (VA) domain.

24-MAR-2003 (first entry)

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ALIGNMENTS

RESULT 1 AAE32500

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AAE32500 standard; protein; 180 AA

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The invention relates to Willebrand Factor A domain related-protein (WARP) which is a member of von Willebrand Factor A (VA)-domain protein superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal constant of the contraction of th
                                                                                                                                                                                                                                                       New isolated Willebrand Factor A-Related Protein polypeptide useful for
the manufacture of a medicament in the treatment of a disease condition
of the extracellular matrix, in particular arthritis.
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                                                                                                                                                                                         Claim 7; Page 72-73; 103pp; English.
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ABU54469

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subject, monitoring repair, regeneration or other disease processes in ar animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The present sequence is human VA domain
                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; cardiovascular disorder; bregnancy-related disorder; cell culture; chemotaxis; food additive; binding partner identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 180
                              Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer' Parkinson's diseases and cancers.
                                                                                            N-PSDB; AAF91860
                                                                                                                                                                                                                                      03-SEP-1999;
03-SEP-1999;
                                                                                                                                                                                                                                                                                    31-AUG-2000; 2000WO-US024008
                                                                                                                                                                                                                                                                                                                                                 WO200118022-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gene 3 encoded secreted protein HNTEO78,
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                                                                                                                                          Baker KP, 1
DR, Young I
PA, Shi Y,
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99US-0152317P.
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                                                                                                                                      se CE, Fiscella M,
Ebner R, Duan DR,
i Y, Florence יי
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Pred. No. 1.6e-94;
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Olsen HS,
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.eur DW;
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Claim 11; Page

532-533; 607pp; English

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RESULT 3
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CC alleviating symptoms associated with the disorders mentioned above, and in disgnostic immunosorbent assay (ELISA). The present sequence represents a human cC secreted protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF91858-AAF91929 represent cDNAs corresponding to protein genes, and AAB87342-AAB87413 represent the AAB87414-AAB87454 represent human secreted protein
                                                                                                                                                                          Albumin fusion protein; therapeutic protein X; human albumin; lhuman serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder;
                                                                                                                cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
                                                                                                                                                                                                                                                                                                                          27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                           ABG65347 standard; protein; 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                         Homo sapiens
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Best Local
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                                                                                                                                    antiasthmatic; anti-HIV; immunosuppressive; antiinflammatory, antipsoriatic; antibacterial; osteopathic; dermatological; antipout immunomodulator; antiarrhythmic; cardiant; nootropic; antilipaemic; nephrotropic; uropathic; neuroprotective; antiparkinsonian; tranqui
                                                                                                                                                                                                                                                                                                                     Albumin fusion
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
                                                                                                         nephrotropic; uropathic; neuroprotective; antiparkinsonian; tranquiliz antidiabetic; anabolic; hypertensive; vulnerary; gene therapy; cancer;
                                                                                                                                                                                                                                                            albumin fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADL78614 standard;
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                           Unidentified
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anti-HIV;
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Pred. No. 2e-94;
; Mismatches 0;
                                                                                    therapeutic
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                                                                                    protein
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                                                                                                                                                                                                                                                            antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 215;
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                                                                                                                                                                                                      antigout;
                                                                                                                                                tranquilizer;
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cc cardiant, noctropic, antilipaemic, nephrotropic, uropathic, anabolic, cardiant, noctropic, antilipaemic, nephrotropic, uropathic, anabolic, compresentive, and vulnerary. The albumin fusion protein nucleic acid may compresent in gene therapy to treat disorders. The albumin fusion protein is useful for diagnosing, treating, preventing or ameliorating diseases or disorders comprising indication: Y. The diseases or disorders include: cancer (e.g. leukaemia, colon, bone, breast, liver or lung cancer), commune or haematopoietic diseases (e.g. anaemia, Hodgkin's disease, acute limmune or haematopoietic diseases (e.g. arthritis, asthma, AIDS, cardiomune disease, inflammatory bowel disease, psoriasis or Lyme CC autoimmune disease, inflammatory bowel disease, psoriasis or Lyme CC disease), reproductive system disorders (e.g. prostatitis, inguinal hernia, varicocele, penile carcinoma, ovarian adenocarcinoma or Sertoliclydig tumours), musculoskeletal disease (e.g. giant cell tumours, CC laydig tumours), musculoskeletal disease (e.g. rhabdomyomas, heart disease, garrhythmia, cardiac arrest, heat valve disease, hypernatraemia or carchevia), misculos arrest, heat valve disease, hypernatraemia or carchevia, miscular arrest, heat valve disease, hypernatraemia or carchevia disease arrest, heat valve disease, hypernatraemia or carchevia disease (e.g. rhabdomyomas, heart disease).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorder in a patient comprising the step of administering the albumin fusion protein; a method of treating a patient with a disease or disorder that is modulated by Therapeutic protein: X, or its fragment or variant; a method of extending the shelf life of Therapeutic protein: X, or its fragment or variant; a nucleic acid molecule comprising a polynucleotide sequence encoding the albumin fusion protein; a vector comprising the nucleic acid molecule of the albumin fusion protein; and a host cell comprising the nucleic acid molecule of the albumin fusion protein. The albumin fusion protein and its compositions have the following activities: cytostatic, antianemic, antiarthritic, antiasthmatic, antischmatic, dermatological, antigout, immunoscoplator, antiarrhythmic, nartigout, nartigout, immunoscoplator, antiarrhythmic, partigon, antigout, immunoscoplator, antiarrhythmic, partigon, carrier antilinearic nantiarrhythmic, immunoscoplatic, dermatological, antigout, immunoscoplator, antiarrhythmic, partigon, antigout, antigout, immunoscoplator, antiarrhythmic, partigon, antigout, antig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-APR-2000;
25-APR-2000;
21-DEC-2000;
                                                                                                                                                                  compulsive disorder), respiratory disease (e.g. emphysema, lung cancer occupational lung disease), endocrine diseases (e.g. diabetes, Addison' disease or glomerulonephritis), digestive diseases (e.g. portal hypertension, irritable bowel disease, gastric atrophy or pancreatitis) or connective tissue or epithelial diseases (e.g. Crohn's disease, scleroderma, wound healing or epidermolysis bullosa). This sequence
                                                                                                                                                                                                                                                                                                                                                                         hyponatraemia), mixed foetal diseases (e.g. foetal alcohol syndrome, Down's syndrome, Patcau syndrome, Turner's syndrome, Apert syndrome or T. Sachs disease), excretory disease; ce.g. urinary incontinence, urinary tract infections or renal disorders), neural or sensory disease (e.g. Alzheimer's disease, Parkinson's disease, cerebral malaria, meningitis, cerebellar ataxia, attention deficit disorder, autism or obsessive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New albumin fusion proteins, useful for diagnosing, treating, preventing or ameliorating diseases or disorders e.g. cancer, anemia, arthritis, asthma, inflammatory bowel disease or Alzheimer's disease.
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                                                                                                   represents a therapeutic protein X relating of the invention. The sequence listing
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HASELTINE W A.
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Best Local
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AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87342-AAB87413 represent the proteins they encode. AAB87414-AAB87454 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the protein in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of
                                                                                                                                                                                                                    Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers.
                                                                                                                                                                                  Disclosure; Page 18; 607pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      03-SEP-1999;
03-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gene 3 encoded secreted protein fragment, SEQ ID NO:165
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                                                                                                                                                                                                                                                                                                                                                    Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    secreted protein; proliferative disorder; cancer; tumour;
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                                                                                                                                                                                                                                                                                                                    Young PE,
Shi Y, Wei
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99US-0152317P.
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Y, Florence
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er R, Duan DR,
Florence KA;
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Pred. No. 2e-94;
; Mismatches
                                                                                                                                                                                                                                                                                                                                  Komatsoulis GA,
Olsen HS, Laf
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gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein fragment referred to in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            appormainties, haematopoietic disorders, diseases of the immu AIDS, autoimmune diseases (e.g., rheumatoid arthritis), infil allergies, neurological disorders (e.g., Alzheimer's disease partingons's discount descriptions (e.g., Alzheimer's disease)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkinsons's disease), cognitive disorders, schizophrenia, asthmodisorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders
Sequence
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     226
     AA;
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                 121 GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD
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GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD
                                                                    SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
                                                                                                                                          RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH 104
                                  180
                                                                    164
224
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Matches Query Match

Local 180;

Similarity

100.0%;

Score 913; DB 4; Pred. No. 2.2e-94; Mismatches

Length Indels

Conservative

0;

0,

0

Gaps

AAB87418 ID AABE XX RESULT 6 AAB87418 standard; (first entry) protein;

Human gene 3

encoded secreted protein fragment, SEQ

ij

NO:159

foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; cell culture; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food WO200118022-A1 Homo sapiens. secreted protein; proliferative disorder; cancer; tumour; partner

31-AUG-2000; 2000WO-US024008

03-SEP-1999; 03-SEP-1999; 99US-0152315P. 99US-0152317P.

(HUMA-) HUMAN GENOME SCI INC

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RESULT 7
AAB88340
ID AAB8
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DE Huma
XX
KW Huma
KW rheu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC proliferative disorders, cancer, tumours, foetal and developmental CC abnormalities, haematopoietic disorders, diseases of the immune system, CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, CC allergies, neurological disorders (e.g., Alzheimer's disease, CC allergies, neurological disorders (e.g., Alzheimer's disease, CC allergies, neurological disorders, schizophrenia, asthma, skin CC disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, CC gastrointestinal disorders, pregnancy-related disorders, endocrine CC disorders, and infections. The proteins can also be used to aid wound CC disorders, and epithelial cell proliferation, to prevent skin aging due to CC sumburn, to maintain organs before transplantation, for supporting cell CC culture of primary tissues, to regenerate tissues, to identify their CC cognate ligands or binding partners, and in chemotaxis, and can be used CC as a food additive or preservative to modify storage properties.

CC Antibodies specific for a protein of the invention can be used in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked CC immunosorbent assay (ELISA). The present sequence represents a human CC secreted protein fragment referred to in the discolosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Soppet DR, You
Moore PA, Shi
Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 242 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87342-AAB87413 represent the proteins they encod AAB87414-AAB87454 represent human secreted protein fragments. The gene and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 18; 607pp; English
                                                                                                        Human membrane or secretory protein clone PSEC0053.
                                                                                                                                                                                   23-MAY-2001
                                                                                                                                                                                                                                                                                                                             AAB88340 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
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Young PE, Ebner R, Duan DR,
Shi Y, Wei Y, Florence KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                     protein; 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 913; DB 4; 100.0%; Pred. No. 2.4e-94; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                             B
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Olsen HS, Laf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 242;
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Lafleur DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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- AAB8419. Included in the invention are primers AAF9317 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the cinvention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polymucleotide sequences can be used in gene therapy. The polymucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The
                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding secretory proteins/membrane proteins, useful gene therapy or as candidate target molecules in drug development.
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02-MAY-2000; 2000JP-00183766.
                                                                                                                                                                                                                                                                                                                     Sequence 285 AA;
                                                                                                                                                                                                                                                                                                                                                                             polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to nucleic acid sequences AAF93744 - AAF93916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-093989/11.
N-PSDB; AAF93767.
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                                                                                                                                                                                                                                                                                                                                                            treated include rheumatoid arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JAN-2000;
                                   121
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                  GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEXHLHFVDVDDLHIIVQELRGSILD 180
                                                                                                                                                                                RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
                                                                          SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
                                                                                                 SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 120
                                                                                                                                                           RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO
GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD
                                                                                                                                                                                                                                    100.0%; ilarity 100.0%; Conservative (
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                                                                                                                                                                                                                                    Score 913; DB 4
Pred. No. 3e-94;
); Mismatches
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                                                                                                                                                                                                                                                                                                                                                            diabetes
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                                                                                                                                                                                                                                                                           Length 285;
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RESULT 8
ADY63045
ID ADY6
XX
AC ADY6

ADY63045 standard; protein; 285 AA

151

211

91

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ADY63045;

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RESULT 9
AAE32502
ID AAE3
XX
AC AAE3
XC AAE3
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DT 24-M
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                                                                                                                                                                                                                                                                                                                                                            membrane proteins, and their coding sequences. The present sequence is one such protein sequence. The coding sequences of the invention are useful for examination and diagnosis of abnormality of the human secretary proteins and in gene therapy methods. The coding sequences and proteins are useful as candidates for medicines or as target molecules for developing medicines. Antibodies against the proteins of the invention are useful for treating diseases that are associated with the proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained from sequence information supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The
  Human
                         24-MAR-2003
                                                  AAE32502
                                                                         AAE32502 standard;
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 48; 1240pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated polynucleotide encoding human membrane proteins, useful for examination and human secretary proteins.
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02-MAY-2000;
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                                                                                                                                                                                                                                                                                                      Local
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  Willebrand
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                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                         285
                                                                                                                                      GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD
                                                                                                                                                   GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD
                                                                                                                                                                                                        SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
                                                                                                                                                                                                                                        RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
                                                                                                                                                                                                                                                     RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
                                                                                                                                                                                       SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
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ilarity 100.0%;
Conservative (
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2000JP-00183766.
2000EP-00114090.
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                         (first entry)
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  Factor
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 A domain related-protein
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Pred. No. 3e-94;
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                                                                                                                                                                                                                                                                                         Mismatches
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diagnosis
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   (WARP)
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s of abnormality
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GPPMQELKDLGVTVFIVSTGRGNELELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD

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                                                                                                        Matches
                                                                                                                                                                                              The invention relates to Willebrand Factor A domain related-protein (WARP) which is a member of von Willebrand Factor A (VA)-domain protein superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The
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                                                                                                                                                           Sequence
                                                                                                                                                                                     present sequence is
                                                                                                                                                                                                                                                                                                                                                                      New isolated Willebrand Factor A-Related Protein polypeptide useful for the manufacture of a medicament in the treatment of a disease condition of the extracellular matrix, in particular arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200288184-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pept ide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MURD-)
                                                                                                                                                                                                                                                                                                                                                                                                                                         2003-111873/10
                                                                                                        180;
                                                    32
                                                                                                                                                                                                                                                                                                                                               11; Page 76-78;
 92
                          61
                                                                            Н
                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MURDOCH CHILDRENS RES
                                                                                                                                                                                                                                                                                                                                                                                                                             AAD50399
                                                                                                                                                            418
                   SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
                                                                 RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
                                                    RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
 SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fitzgerald
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "0-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "N-glycosylation site"
                                                                                                                                                                                     human WARP protein
                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "O-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Human mature WARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
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                                                                                                        0;
                                                                                                     Score 913; DB 6;
Pred. No. 5.2e-94;
; Mismatches 0;
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                                                                                                                                 Length 418;
                                                                                                        Indels
                                                                                                        0
                                                                                                        Gaps
                           120
  151
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152

GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD 211

RESULT 10

ABP69674;

ABP69674 standard;

protein; 445 AA.

180 211

151

120 91

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The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ11119-CC ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences: The polynucleotides are useful for central protein or complementary sequences: The polynucleotides are useful for cencoded polypeptides (ABP68902-ABP69849) are useful as molecular weight cencoded polypeptides (ABP68902-ABP69849) are useful as molecular weight cencoded polypeptides (ABP68902-ABP69849) are useful as molecular weight comarkers, as a food supplement, for generating antibodies; in medical comparing, screening and diagnostic assays and for treating cell-cc proliferative disorders (cancer), neurodegenerative diseases (Parkinson's cor Alzheimer's disease), autoimmune diseases (multiple sclerosis, cor Alzheimer's disease), autoimmune diseases (multiple sclerosis, cor alzheimer's disease), autoimmune diseases (multiple sclerosis, cor alzheimer's diseases), autoimmune diseases (multiple sclerosis, cor alzheimer's diseases), autoimmune diseases (multiple sclerosis, cor alzheimer's diseases, autoimmune diseases, autoimmune diseases (multiple sclerosis, cor alzheimer's diseases, a
                                                                          Matches 180;
                                                                                                    Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infectio arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoa;
                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; SEQ ID NO 1721; 1012pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAR-2001; 2001US-00799451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAR-2002; 2002WO-US005095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coagulation disorders.
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                                                                                                    Similarity
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Yang Y, Ma
T, Wang J,
                                                                                                                                                                            445
RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goodrich RW, Asundi V, Z.
Ma Y, Yamazaki V, Chen R,
Wang D, Drmanac RT;
                                                                                                    100.0%;
                                                                          0
                                                                                                 Score 913; DB 5;
Pred. No. 5.7e-94;
                                                                          Mismatches
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R, Wang Z,
                                                                             0:
                                                                                                                        Length 445;
                                                                             Indels
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RESULT 11
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12-JUN-
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vaccine; cancer; cachexia; Alzheimer's
obesity; diabetes; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-2002
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05-JUN-2002;
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2002US-0389118P
2002US-0389144P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       betic; antimicrobial; antilipaemic; gene therapy;
achexia; Alzheimer's disease; Parkinson's disease;
infectious disease; metabolic syndrome X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunomodulator;
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09-AUG-2002;
09-AUG-2002;
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2002US-0402811P
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2002US-0403459P
2002US-0403531P
2002US-0403531P
2002US-0403531P
2002US-0406182P
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2002US-0423139P
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(CURA.

Alsobrook JP, ...

I Catterton E, Chapova.
Eltenberg S, Gangolli EA,
Gusev VY, Herrmann JL, Ji W,
Archlan T, Malyankar UM, M
Patturajan M, Pe
"henberg ME, S
"KA, Sto Rieger DK, Smithson G Zhong H; Rothenberg ME, Sci Spytek KA, Stone Alvarez E, Anderson DW, Boldog FL, Casm Chapoval A, Crabtree-Bokor JR, Edinger SI Gangolli EA, Gerlach VL, Gorman L, Guntl rrmann JL, Ji W, Kekuda R, Li L, Liu X, Walyankar UM, Mezick AJ, Millet I, Miel Patturajan M, Pena CEA, Peyman JA, Raha I othenberg ME, Sciore P, Shenoy SG, Shimke Spytek KA, Stone DJ, Vernet CAM, Voss EZ. Boldog FL, Casman SJ; ir JR, Edinger SR, Ellerman Gorman L, Gunther E, Guo X L, Li L, Liu X, Macdougall Shimkets RA; Raha D, Mishra VS; EZ, Rastelli L; 3 JR; 7.

2004-081935/08

treating NOVX polypeptides and nucleic acid molecules useful for preventing NOVX-associated disorders, e.g. cancer, diabetes, infection or and in chromosome mapping, tissue typing or pharmacogenomics. 9

SEQ ID NO 2; 1880pp; English.

antilipaemic activity, and may have a use in gene therapy, and as a vaccine. The polypeptides are encoded by NOVX polynucleotides comprising any of the 303 fully defined nucleotide sequences given in the specification. The polypeptide is useful in the manufacture of a medicament for treating a syndrome associated with a human disease. The polypeptide, polynucleotide and antibody are useful in diagnosing, treating or preventing NOVX-associated disorders, e.g. cancer, cachexia, Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are The invention relates to a novel isolated polypeptide (NOVX). A polypeptide of the invention has cytostatic, immunomodulator, neuroprotective, nootropic, anorectic, antidiabetic, antimicrobine hybridisation probes, chromosome mapping, tissue antimicrobial, and

MR,

DAM,

Shah

Au-Young

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RESULT 12 AAE03654 Ş 밁 Ş Ś SSSS 밁 Matches Query Match Best Local Yue H, Baughn inflammatory disorder; acquired immune deficiency syndrome; AIDS; Addison's disease; allergy; anaemia; asthma; atherosclerosis; melanoma; Crohn's disease; allergy; anaemia; concer; glomerulonephritis; multiple sclerosis; Grave's disease; osteoarthritis; glomerulonephritis; multiple sclerosis; Grave's disease; osteoarthritis; Human; extracellular matrix and cell adhesion molecule; XMAD; gene therapy; genetic disorder; adrenoleukodystrophy; leukaemia; gene therapy; genetic disorder; adrenoleukodystrophy; leukaemia; bomn's syndrome; cystic fibrosis; Gaucher's disease; myotonic dystrophy; sickle cell anaemia; thalassaemia; autoimmune disorder; adenocarcinoma; AAE03654 standard; protein; 185 Region arteriosclerosis; osteoporosis; psoriasis; rheumatoid arthritis; ulcerative colitis; infection; cell proliferative disorder; actinic keratosis; myeloma; 06-AUG-2001 typing, preventive medicine, and pharmacogenomics. represents a NOVX polypeptide of the invention. 05-DEC-2000; WO200142285-A2 Region Region Region Homo sapiens neuroprotective; 152 121 180; extracellular matrix and cell adhesion molecule-18 (XMAD-18) 92 61 32 ш Tang YT, INCYTE GENOMICS Similarity RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH 445 GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 120 ${\tt RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH}$ 5 Conservative A, 2000WO-US032990 (first entry) 99US-0172852P 99US-0172354P /note= /note= ; nootropic; anticonvulsant; antithyroid; nephrotropic; dermatological. /note= Location/Qualifiers 03 Lal P, .170 100.0%; "Collagen glycoprotein "Collagen glycoprotein precursor" "Collagen glycoprotein precursor" "Collagen glycoprotein precursor" INC. Burford N, 1 P, Au-Youn 0 Willebrand Score 913; DB 8; Pred. No. 5.7e-94 A Mismatches Azimzai Y, factor domain score" ٥, precursor" Length Patterson Indels The present sequence Ç 0 180 211 151 91 60

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RESULT 13
AAB42581
ID AAB42
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AC AAB42
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O8-FE
DT 08-FE
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DE Humar
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KW Humar
KW vulne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC hybridisation probe useful in mapping the naturally occurring genomic CC sequences and to create knock in humanised animals (pigs) or transgenic CC animals (mice or rats) to model human diseases. Oligonucleotide or longer CC fragments derived from the polynucleotide sequences may be used as CC used for the diagnosis of disorders which specifically bind XMAD may be used for the diagnosis of disorders which specifically bind XMAD may be CC used for the diagnosis of disorder which specifically bind XMAD may be CC disease, prevented or treated include genetic disorders such as CC disease, mystonic dystrophy, Down's syndrome, cystic fibrosis, Gaucher's CC disease, mystonic dystrophy, sickle cell anaemia, thalassaemia, CC autoimmune/inflammatory disorders such as acquired immune deficiency CC syndrome (AIDS), Addison's disease, allergies, anaemia, asthma, CC steeporosis, Crohn's disease, diabetes mellitus, atopic dermatitis, CC osteoporosis, psoriasis, rheumatoid arthritis, ulcerative colitis, osteoporosis, psoriasis, rheumatoid arthritis, ulcerative colitis, parasitic, protozoal and helminthic infections and CC and cancer including breast, bladder, bone marrow, brain and uterus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            molecule (XMAD). The XMAD is used for screening a compound for effectiveness as an agonist or antagonist of XMAD. The identified agonist or antagonist are used for treating a disease or condition associated with decreased or increased expression of functional XMAD. The polynucleotides encoding XMAD are useful in somatic or germline gene therapy to correct a genetic deficiency, to express a conditionally lethal gene product and to express a protein which affords protection against intracellular parasites and also for diagnosis of disorders associated with expression of XMAD. They are also used for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human extracellular matrix and cell adhesion molecules and polynucleotide sequences encoding them, useful for diagnosis, prevention, treatment of genetic, autoimmune and cell proliferative disorders.
                    Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nostropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
                                                                                                                                                                                                                                                                   AAB42581 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer, leukaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 111; 135pp; English.
                                                                                                                                                                             08-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQDAVRASAQRMGDTHTGLALVYAKEQLEAEASGARPGVPKVLVWVTDGGSSDPVGPPM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPVGPPM
                                                                                                                                 ORF2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adenocarcinoma, lymphoma,
                                                                                                                                 polypeptide
                                                                                                                                                                           entry)
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is a human extracellular matrix and cell adhesion
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Pred. No. 3.
                                                                                                                                   sequence
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                                                                                                                                   SEQ ID
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                                                                                                                                   NO:4690
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, disorders, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
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05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; ast allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antianaemic; gene therapy; cancer; proliferative disorder; hyperte neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; A
                                                                                                                                                                                                                                                                               Sequence 299
                                                                                                                                                                                                                                                                                                                                     disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 3880-3881; 5507pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiviral; antibacterial; antifungal; antirheumatic;
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                                                                                                                                                                                                                                                                                                                      coagulation;
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                                                                                                                                                      DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS
                                                                                GBAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVMVTDGGSSDPVGP 122
PMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD
                                                        GEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPVGP
                                                                                                                                  DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLAPXALRASLVHVGSRPYTEFPFGQHSS
                                                                                                                                                                                                        Conservative
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99US-0127728P.
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                                                                                                                                                                                                                      96.7%;
98.3%;
                                                                                                                                                                                                                                                                                                                    to inhibit thrombosis;
                                                                                                                                                                                                       0
                                                                                                                                                                                                                        Score 883; DB 3
Pred. No. 8e-91;
                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                      and as a contraceptive
                                                                                                                                                                                                                                          Length 299;
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PMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD

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Best Local
                                                                                                                                                                                                                                                                             animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The
                                                                                                                                                                                                                                                                                                                                                  The invention relates to Willebrand Factor A domain related-protein (WARP) which is a member of von Willebrand Factor A (VA)-domain protein superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an
                                                                                                                                                                                                                                      Sequence 180 AA;
                                                                                                                                                                                                                                                                 present sequence is mouse VA domain
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 78-79; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bateman JF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the extracellular matrix, in particular arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isolated Willebrand Factor A-Related Protein polypeptide useful for manufacture of a medicament in the treatment of a disease condition {\bf r}
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 121
                             121
                                                                                                                                                                             150;
                                                            61
                                                                                      61
                                                                                                                                                1-1
                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MURDOCH CHILDRENS RES INST
                                                                                                                                    RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
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                    GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIVQELRGSILD
                                                            SSGQAIRDAIRVAPQRMGDTNTGLALAYAKEQLFAEEAGARPGVPKVLVWVTDGGSSDPV
                                                                                      SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
                                                                                                                   QGDLLFLLDSSASVSHYEFSRVREFVGQLVATMSFGPGALRASLVHVGSQPHTEFTFDQY
   GPPMQELKDLGVTIFIVSTGRGNLLELLAAASAPAEKHLHFVDVDDLPIIARELRGSITD
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fitzgerald
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                                                                                                                                                                                           84.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Encoded by GGG"
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                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  related-protein; von Willebrand Factor A; VA; molecular marker; cartilage; arthritis; WARP;
                                                                                                                                                                                          Score 768; DB 6
Pred. No. 4e-78;
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                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                        6; Length 180
                                                                                                                                                                             16;
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                                                                                                                                                                                                                                                                                                                             invention is
                                                                                                                                                                            Gaps
                             180
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AAESJLIT 15
AAESJ2501
XX AAESJ2501
XX AAESJ2501
AC AAESJ2
AC AAESJ
                                                  The invention relates to Willebrand Factor A domain related-protein (MARP) which is a member of von Willebrand Factor A (VA)-domain protein superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The present sequence is mouse WARP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Willebrand Factor A-Related Protein polypeptide useful for
the manufacture of a medicament in the treatment of a disease condition
of the extracellular matrix, in particular arthritis.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAY-2001; 2001AU-00004701
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84.1%; Score 768; DB 6; 83.3%; Pred. No. 1.3e-77; tive 14; Mismatches 16

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Length 415;

Search completed: Pebruary 13, 2006, 07:39:50 Job time : 112.565 secs

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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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US-10-883-936-85
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US-10-699-035A-20
US-10-699-035A-31
US-10-699-035A-31
US-10-699-035A-21
US-10-699-035A-25
US-10-177-293-61
US-10-301-822-63
US-10-631-467-998
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Sequence 2, Appli
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121 GPPMOELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVDDLHIIV	Query Match Best Local Similarity 100.0%; Score 913; DB 4; Length 180; Best Local Similarity 100.0%; Pred. No. 1.5e-89; Matches 180; Conservative 0; Mismatches 0; Indels 0; G QY 1 RGDLMFLLDSSASVSHYEFSRVREFVQQLVAPLPLGTGALRASLVHVGSRPYTEFP Db 1 RGDLMFLLDSSASVSHYEFSRVREFVQQLVAPLPLGTGALRASLVHVGSRPYTEFP OY 1 RGDLMFLLDSSASVSHYEFSRVREFVQQLVAPLPLGTGALRASLVHVGSRPYTEFP OF 1 SGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEAGGARPGVPKVLVWVTDGGS	RESULT 1 US-10-699-035A-2 Sequence 2, Application US/10699035A Publication No. US20040214349A1 GENERAL INFORMATION: APPLICANT: Bateman, John APPLICANT: Fitzgerald, David TITLE OF INVENTION: A Molecular Marker FILE REFERENCE: A36056 PCT USA A 071838.0142 CURRENT APPLICATION NUMBER: US/10/699.035A CURRENT FILING DATE: 2003-10-31 PRIOR APPLICATION NUMBER: PCT/AU02/00542 PRIOR FILING DATE: 2002-05-02 PRIOR FILING DATE: 2001-05-02 INUMBER OF SEQ ID NOS: 40 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 180 TYPE: PRT ORGANISM: Homo sapiens	28 256.5 28.1 755 3 US-09-919-497-57 29 256.5 28.1 1780 4 US-10-115-479-10 Sequence 30 254.5 27.9 1207 4 US-10-408-765A-1591 Sequence 31 254.5 27.9 1297 4 US-10-000-512-8 32 251.5 27.5 776 4 US-10-000-512-8 Sequence 33 251.5 27.5 776 4 US-10-074-566-8 Sequence 34 251.5 27.5 782 4 US-10-074-566-8 Sequence 35 251.5 27.5 782 4 US-10-04-378A-16 Sequence 36 251.5 27.5 896 4 US-10-04-378A-16 Sequence 37 251.5 27.5 896 4 US-10-428-275-158 Sequence 38 251.5 27.5 896 4 US-10-428-275-158 Sequence 39 251.5 27.5 915 3 US-09-909-308B-34 Sequence 40 251.5 27.5 915 3 US-09-909-88B-34 Sequence 41 251.5 27.5 915 3 US-09-907-824-34 Sequence 42 251.5 27.5 915 3 US-09-907-824-34 Sequence 43 251.5 27.5 915 3 US-09-907-824-34 Sequence 44 251.5 27.5 915 3 US-09-907-824-34 Sequence 45 251.5 27.5 915 3 US-09-907-824-34 Sequence 46 251.5 27.5 915 3 US-09-907-824-34 Sequence 47 251.5 27.5 915 3 US-09-907-824-34 Sequence 48 251.5 27.5 915 3 US-09-907-824-34 Sequence 49 251.5 27.5 915 3 US-09-907-824-34 Sequence 40 251.5 27.5 915 3 US-09-907-824-34 Sequence 41 251.5 27.5 915 3 US-09-907-824-34 Sequence 42 251.5 27.5 915 3 US-09-907-824-34 Sequence 43 251.5 27.5 915 3 US-09-907-824-34 Sequence 44 251.5 27.5 915 3 US-09-907-824-34 Sequence 45 251.5 27.5 915 3 US-09-907-824-34 Sequence
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TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
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COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino US-09-789-561-85
                                                                                                                                                                                            ; OTHER INFORMATION: US-09-833-245-2096
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Best Local Similarity 100.
Matches 180; Conservative
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PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
NUMBER: 05 SEQ ID NOS: 194
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TYPE: PRT
ORGANISM: Homo F
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SEQ ID NO 85
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                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                         RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
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Pred. No. 1.9e-89;
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                                                            CURRENT APPLICATION NUMBER: US/09/789,561
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR PILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
                                                                                                                                                                                                                                                                                                           Sequence 165, Application US/09789561
Patent No. US20020064818A1
GENERAL INFORMATION:
SOFTWARE: P
SEQ ID NO 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                            APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: PZ043P1
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PRIOR TIING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
SOFTWARE: Patentin Ver. 2.0
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PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
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NAME/KEY: SITE
LOCATION: (7)
                                         NUMBER OF SEQ ID NOS:
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ORGANISM: Homo
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Pred. No. 1.9e-89;
); Mismatches 0;
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RESULT 7
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                                              Sequence 159, Application US/09789561 Patent No. US20020064818A1 GENERAL INFORMATION:
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SEQ ID NO 165
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GENERAL INFORMATION:
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Best Local Similarity
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PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
           APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted proteins
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NUMBER OF SEQ ID NOS: 194
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ORGANISM: Homo sapiens
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PZ043P1
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100.0%; Pred. No. 2e-89;
ative 0; Mismatches 0;
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US-10-883-936-159
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CURRENT FILING DATE: 2001-02-22
PRIOR *PEPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/883,936
CURRENT FILING DATE: 2004-07-06
PRIOR APPLICATION NUMBER: US/09/789,561
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR PPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
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                                                                                                                                                                               SOFTWARE: PatentIn
SEQ ID NO 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 159, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: PZ043P1
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                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
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OTHER INFORMATION:
NAME/KEY: SITE
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NAME/KEY: SITE
                                     OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                        NAME/KEY: SITE LOCATION: (2)
                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                         TYPE:
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ORGANISM: Homo
NAME/KEY: SITE
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                     FEATURE:
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                                                                                                                                                            ENGTH: 242
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Pred. No. 2.2e-89;
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APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILLING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCTANU02/00542
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
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US-10-699-035A-6
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                                                                                                                                 RESULT 10
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                                                        Sequence 20, Application US/10699035A Publication No. US20040214349A1 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Bateman, John
APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bateman, John APPLICANT: Fitzgerald,
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NAME/KEY: SITE
LOCATION: (34)
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TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 4.7e-89;
Mismatches 0;
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Pred. No. 2.2e-89;
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US-10-149-819-18
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                                                                                                                                                                                                                                                                                 SOFTWARE: PERL Program
SEQ ID NO 18
LENGTH: 185
                                                                                Matches
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                                                                                                                    Query Match
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                                                                                                                                                                             TYPE: PRT
ORCANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyt
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                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/149,819
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/172,852; 60/172,354
PRIOR FILING DATE: 1999-12-10; 1999-12-16
NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BURFORD, Neil TITLE OF INVENTION: EXTRACELLULAR MATRIX AND FILE REFERENCE: PF-0760 PCT
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TYPE: PRT
ORGANISM: Homo sapiens
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mes 180; Conserv
                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 120
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LAL, Preeti
. AU-YOUNG, Janice
. AU-YOUNG, Vanice
. TO FORD, Neil
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TANG, Y. Tom
PATTERSON, Chan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
                     MFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGE
  MFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAUGHN, Mariah R.
LU, Dyung Aina M.
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                                                                            97.7%; So ilarity 100.0%; 1 Conservative 0;
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                                                                                                                                                                                 Incyte ID No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chandra
                                                                              Score 892; DB 4; I
; Pred. No. 2.7e-87;
0; Mismatches 0;
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                                                                                                                  Length 185
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; OTHER INFORMATION: VA domain from WARP US-10-699-035A-31
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                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 181
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 31, Application US/10699035A Publication No. US20040214349A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 8
LENGTH: 180
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TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR FILING DATE: 2002-05-02
                                                                                                                                                                              CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
                                                                                                                                                                                                                                                                                                   APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
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                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/699,035A CURRENT FILING DATE: 2003-10-31
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bateman, John APPLICANT: Fitzgerald,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Mus musculus
                                        FEATURE:
                                                           ORGANISM: Artificial Sequence
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Sequence 21, Application US/10699035A

Publication No. US20040214349A1

GENERAL INFORMATION:
APPLICANT: Biteman, John
APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142

CURRENT APPLICATION NUMBER: US/10/699,035A

CURRENT FILING DATE: 2003-10-31

PRIOR APPLICATION NUMBER: PCT/AU02/00542

PRIOR APPLICATION NUMBER: AU PR4701/01

PRIOR APPLICATION NUMBER: AU PR4701/01

PRIOR APPLICATION NUMBER: AU PR4701/01

PRIOR APPLICATION NUMBER: AU PR4701/01
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US-10-699-035A-4
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US-10-699-035A-21
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TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
FILE REFERENCE: A36056 PCT USA A 071838.0142
FURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 4
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Best Local Similarity
Matches, 150; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 150;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 415
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; Pred. No. 5.6e-74;
14; Mismatches 16
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071838.0142

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
                                                                                                                                             Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                 seq length: 0
seq length: 2000000000
Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PETCOMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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537.392 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	è	ű	4	ω	2	1	Result No.
	233.5								251.5			٠	٠				•	251.5		٠	251.5		•	ū	259	384	Score
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US-08-463-218-1	US-08-897-443-4	US-08-001-078A-1	US-08-463-180-37	US-08-462-128-37	US-08-897-443-3	US-09-949-016-11520	US-09-949-016-11519	US-09-949-016-6215	US-09-906-722A-34	US-09-902-736A-34	US-09-904-462-34	US-09-906-646-34	US-09-906-618-34	US-09-905-381A-34	US-09-909-064-34	US-09-904-920A-34	US-09-903-603A-34	US-09-906-700-34	US-09-902-775A-34	US-09-905-125A-34	US-09-907-794A-34	US-08-897-443-1	US-09-919-497-57	US-09-949-016-10341	US-09-949-016-10340	US-09-513-999C-6277	ID
Sequence 1, Appli	e 4,	e 1	e 37,	e 37,	Sequence 3, Appli	e 115	11519,	Sequence 6215, Ap	Sequence 34, Appl	34,	34,	34,	e 34,	34,	34,	34,	34,	Sequence 34, Appl	34,	34,	w	e 1,	e 57,	Sequence 10341, A	Sequence 10340, A	Sequence 6277, Ap	Description

233.5 25.6 496 4 PCT-US94-00253-1 231.5 25.6 496 2 US-09-914-259-34 221.7 24.9 405 2 US-09-914-259-34 224.5 24.6 481 2 US-09-914-259-36 214.5 23.5 486 2 US-09-914-259-35 214.5 23.5 486 2 US-09-949-016-6216 214.5 23.5 486 2 US-09-949-016-6216 214.5 23.5 1486 2 US-09-949-016-6216 214.5 23.5 20.7 2 US-09-949-016-9878 198.5 21.7 171 2 US-09-996-611D-2 198.5 21.7 954 2 US-09-996-611D-1 194 21.2 214 2 US-10-061-658-6 194 21.2 214 2 US-10-061-658-9 194 21.2 550 2 US-09-905-705A-227 194 21.2 550 2 US-09-906-775A-227	45	44	43	42	41	40	9 9	9 8	37	36	G G	ω 4	ω u	32	31	30	29	6
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	Appli	227, Apr	227, App	227, App	227, App	9, Appli	6, Appli	1, Appli	2, Appli	9878, AL	6216, Ap	278, App	35, App1	36, Appl	374, App	34, App	1, Appli	

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RESULT 2
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; LOCATION: 66
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US-09-513-999C-6277
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            GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                          Sequence 10340, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
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GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.
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nes 76; Conserv
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NUMBER: US/09/949,016
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Pred. No. 4.8e-36;
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
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US-09-949-016-10341
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US-09-949-016-10341
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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TYPE: PRT
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67; Conserv
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    ISVWAARAKEEGIVMYAVGVGKAVEAELREIASEPÄELHVSYAPDFGTMTHLLENLRGSI
                                                                            VGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGSI 178
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US-09-919-497-57
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US-08-897-443-1
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US-09-919-497-57
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APPLICANT: Mutter, George L.
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 57
LENGTH: 755
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Patent No. 6773883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5981263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Matches
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                                                                                                        COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,443
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
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TYPE: PRT
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APPLICANT: Lal,
APPLICANT: Corle
                                    ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Ph
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HUMAN MATRILIN-3 NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Corley, Neil C. APPLICANT: Shah, Purvi APPLICANT: Kaser, Mathew
                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                        STATE:
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                        STREET:
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53; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDP 119
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                                  36,749
                     PF-0348 US
                                                                                                                                                                                                          Version
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ches 72;
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Best Local Similarity
                                                   PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
                                                                                                            FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                              APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: U.L. CNE: 681719
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                                      APPLICATION NUMBER: US 60/143,048 FILING DATE: 1999-07-07
APPLICATION NUMBER: US 60/145,698 FILING DATE: 1999-07-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL----HFVDVDDLHIIVQE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RADLVFIIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTF
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                                                                                                                                                                                                                                                                                                                              Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Tumas, Daniel
                                                                                                                                                                                                                                                     Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Grimaldi, Christopher
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Eaton, Dan L.
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Botstein, David
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32.2%;
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SEQ ID NO 34
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Best Local Similarity
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TYPE: PRT
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                                                                          PPLICANT
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NO. 666437
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                                                                                                                                                                                                                                                                                                                                                                                                                                            175 DSVAEVAAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 RADLVFIIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTF 114
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                                                                                                                                                                                                                                                                                                                                                    Application US/09905125P
                                                   Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                   Fong, b.....
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
                                                                                         Gerritsen, Mary E.
Goddard, A.
                                                                                                                              Gerber, Hanspeter
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Filvaroff, Ellen
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Eaton, Dan L.
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Pred. No. 2e-19;
6; Mismatches
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RESULT 8
US-09-902-775A-34
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                         Matches
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PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
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PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
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TYPE: PRT
ORGANISM: Homo sapiens
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APPLICATION NUMBER: PCT/US99/20944
FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: PCT/US99/23089
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APPLICATION NUMBER: PCT/US99/21547
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APPLICATION NUMBER: PCT/US99/30999
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APPLICATION NUMBER: PCT/US99/30911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US99/28565
                                                                                         175
                                                                                                                               118 DPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL----HFVDVDDLHIIVQE
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                                                                                                                                                                                                                     61 SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARP----GVPKVLVWVTDGGSS 117
                                                                                                                                                                                                                                                                                                                                                     58;
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                                                                                                                                                                                                                                                                                                          1 RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
                                                                                                                                                                                                                                                                                                                                                   h 27.5%; Score 251.5; DB 2;
Similarity 32.2%; Pred. No. 2e-19;
58; Conservative 36; Mismatches 79;
                                                                                                                                                                                                                                                           RADLVFIIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTF 114
                                                                                         DSVAEVAAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQK
                                                                                                                                                                            KRKSEVERAVKRMRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQ 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paoni,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Margaret Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       James
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Timothy A.
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US-09-902-775A-34
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR PPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
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GENERAL INFORMATION:
                                                                                NUMBER OF SEQ
SEQ ID NO 34
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PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
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CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                             PRIOR APPLICATION NUMBER: PCT/US00/00219 PRIOR FILING DATE: 2000-01-05
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PRIOR FILING DATE: 1999-09-08
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PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
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PRIOR APPLICATION NUMBER: PCT/US99/23089
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PRIOR FILING DATE: 1999-11-30
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                 TYPE: PRT ORGANISM: Homo sapiens
                                                              ENGTH: 915
                                                                                                                                                                          FILING DATE: 1999-12-20
                                                                                                                                                                                            FILING DATE: 1999-12-20 APPLICATION NUMBER: PCT
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Grimaldi, Christopher
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Gerritsen, Mary E.
Goddard, A.
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Stewart, Timothy A.
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Mather, Jennie P.
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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                                                                                                           NOS: 423
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US-09-906-700-34
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Best Local
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                        APPLICATION NUMBER: US 60/146,222
APPLICATION NUMBER: US 60/146,222
FILING DATE: 1999-07-28
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                                     APPLICATION NUMBER: PCT/US99/23089
                                                         FILING DATE:
                                                                            APPLICATION NUMBER: PCT/US99/21547
                                                                                                FILING DATE:
                                                                                                                 APPLICATION NUMBER: PCT/US99/21090
                                                                                                                                      FILING DATE:
                                                                                                                                                        APPLICATION NUMBER: PCT/US99/20944
                                                                                                                                                                           FILING DATE: 1999-09-08
                                                                                                                                                                                               APPLICATION NUMBER: PCT/US99/20594
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Mather, Jennie P.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher J.
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Eaton, Dan L.
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Filvaroff, Ellen
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Botstein, David
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art, Timothy A.
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NUMBER: PCT/US99/28214
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PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
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PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
FILE REFERENCE: GNE.1618P2C12
CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT FILING DATE: 2001-07-11
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                                                       ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and
ITILE OF INVENTION: Acids Encoding the Same
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TYPE: PRT
ORGANISM: Homo sapiens
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APPLICATION NUMBER: PCT/US99/28564
FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/30095
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Ashkenazi, Avi
Botstein, David
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                                                                                         Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Stewart, Timothy A.
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Grimaldi, Christopher
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Filvaroff, Ellen
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Hillan, Kenneth, J.
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Pred. No. 2e
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RESULT 11
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; ORGANISM: Homo
US-09-903-603A-34
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Patent No. 6806352
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Best Local (
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PRIOR FILING DATE: 2000-01-05
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LENGTH: 915
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
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FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
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FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US99/30999
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FILING DATE: 1999-11-30
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FILING DATE: 1999-10-05
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APPLICATION NUMBER: US
FILING DATE: 1999-07-07
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APPLICATION NUMBER: PCT/US99/28565
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Ashkenazi, Avi
Botstein, David
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                    Fong, buccas
Gao, Wei-Qiang
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Filvaroff, Ellen
Gerritsen, Mary E
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Eaton, Dan L.
                 Gerber, Hanspeter
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NUMBER OF SEQ ID NOS: 423
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
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PRIOR APPLICATION NUMBER: PCT
PRIOR FILING DATE: 1999-09-13
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PRIOR APPLICATION NUMBER: US 60/145,698
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PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
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CURRENT FILING DATE: 2001-07-13
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APPLICATION NUMBER: PCT/US99/28564
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DPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL----HFVDVDDLHIIVQE
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Chawart, Timothy A.
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Mather, Jennie P.
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Kljavin, Ivar J.
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Grimaldi, Christopher
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                                                                                                                                                                           Score 251.5; DB 2;
pred. No. 2e-19;
6; Mismatches 79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/145,698 FILING DATE: 1999-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/143,048 FILING DATE: 1999-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US00/04414
                                                                     APPLICATION NUMBER: PCT/US99/30911
                                                                                                                                FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/28565
                                                                                                                                                                      APPLICATION NUMBER: PCT/US99/28564
                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US99/28214
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                                                                                     APPLICATION NUMBER: PCT/US99/30095 FILING DATE: 1999-12-16
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                                   APPLICATION NUMBER: PCT/US99/30999
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INVENTION: Secreted and Transmembrane Polypeptides and
INVENTION: Acids Encoding the Same
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Wood, William, I.
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Eaton, Dan L.
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lan, Kenneth, J.
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NUMBER: PCT/US00/00219
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TITLE OF INVENTION: SECTION: ACIDS Encoding the Same TITLE OF INVENTION: ACIDS Encoding the Same FILE REFERENCE: 10466-14; CURRENT EAPPLICATION NUMBER: US/09/905,381A; CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/04414; PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/143,048
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Best Local S
Matches 58
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SEQ ID NO 34
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TYPE: PRT
ORGANISM:
                                                                                             PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                         PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
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FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
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                                                                                                                                                                                                                                                                                                          INVENTION: Secreted and Transmembrane Polypeptides and Nucleic INVENTION: Acids Encoding the Same
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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Wood, William,
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Mather, Jennie P.
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Eaton, Dan L.
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Botstein, David
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LENGTH: 915
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ORGANISM: Homo sapiens
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FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
APPLICATION NUMBER: PCT/US99/30911
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APPLICATION NUMBER: PCT/US00/00219
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APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
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FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
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APPLICATION NUMBER: PCT/US99/30999
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58; Conservative
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                                                                                                                                                                                                                                                                                         Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL----HFVDVDDLHIIVQE 173
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                                                                             Kljavin, Iva.
Wather, Jennie P.
                                                                                                     Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
                                                                                                                                                                                                                                           Fong,
                                                                                                                                                                                                                                                          Ferrara, Napoleone Filvaroff, Ellen
Williams,
              Stewart, Timo
Tumas, Daniel
                          Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                   Godowski, Paul J.
Grimaldi, Christopher
                                                                                                                                                                                              Gerritsen, Mary E.
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                                                                            James
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APPLICANT:

Desnoyers,

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RESULT 15
US-09-906-646-34
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Sequence 34, Application US/09906646
Patent No. 6852848
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR PRIOR
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
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PRIOR APPLICATION NUMBER: PCT
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT
PRIOR FILING DATE: 1999-10-05
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PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 2000-02-22
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CURRENT FILING DATE: 2001-07-16
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PRIOR FILING DATE: 2000-01-05
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PRIOR FILING DATE: 1999-11-29
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ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 915
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APPLICATION NUMBER: PCT
FILING DATE: 1999-12-20
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                                                                                                                                                                                                                                                                  DPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL----HFVDVDDLHIIVQE 173
                                                                                                                                                                                                                                                                                                              KRKSEVERAVKRMRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQ 174
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nilarity 32.2%;
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Pred. No. 2e-19;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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                                                                                                                                        ; SEQ ID NO 34
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-646-34
                                                            Query Match 27.5%;
Best Local Similarity 32.2%;
Matches 58; Conservative 3
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR
PRIOR
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PRIOR APPLICATION NUMBER: 110 6
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CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-02-22
PRIOR PPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
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PRIOR FILING DATE: 1999-07-07
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PRIOR FILING DATE:
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FILING DATE: 2000-01-05
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APPLICATION NUMBER: PCT/US99/20594
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1 RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH 60
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Stewart, Timothy A.
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Mather, Jennie P.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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                                                            ; Score 251.5; DB 2;
; Pred. No. 2e-19;
36; Mismatches 79;
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Search completed: February 13, 2006, 07:50:51 Job time : 28.6923 secs

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Post-processing: Minimum Match 0%
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2154
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	. 16	15	14	13	12	11	10	9	89	7	6	G	4	ω	2	ם	NO.	Result	•
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A32160	S19694	G00039	A45638	RWHU1C	S42373	A32230	S00551	RWHU1B	A43908	T23760	A48569	A88396	A35854	A45226	A55348	T46488	CGHU3A	A37979	A37797	S66522	A33809	A40970	I51027	A45974	S78476	S31212	A54849	A40020	ID		
tenascin-C - human	tenascin precursor	von Willebrand fac	immunodominant mic	cell surface glyco	hypothetical prote	tenascin precursor	leukocyte surface	cell surface glyco	ronectin -	т	antigen Em100 - Ei	10.2	integrin alpha-1 c	integrin alpha-1 c	integrin alpha-1 -	hypothetical prote	alpha 3(e matrix	ılpha 3 (matrix	matrix	undulin 1 - human		alpha 1	alpha	alpha	alpha 1	collagen alpha 1(X	Description	•	

A;Molecule type: mRNA, A;Molecule type: mRNA, A;Residues: 2960-2976, F',2978-3074, 'AG' <GOR3> A;Residues: 2960-2976, F',2978-3074, 'AG' <GOR3> A;Cross-references: UNIPARC:UPI00001712F4; EMBL.M17375; NID:g211649; PIDN:AAA48718.1; PA;Note: this sequence has been revised in reference A34485 R;Koch, M.; Bernasconi, C.; Chiquet, M. R;Koch, M.; Bernasconi, C.; Chiquet, M. Biochem. 207, 847-856, 1992 Eur. J. Biochem. 207, 847-856, 1992 A;Title: A major oligomeric fibroblast proteoglycan identified as a novel large form of A;Reference number: S23814; MUID:92362621; PMID:1323460

R;Gordon, M.K.; Gerecke, D.R.; Olsen, B.R. Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987 A;Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA of A;Reference number: A28037; MUID:87317590; PMID:3476925

Accession: A28037

R;Dublet, B.; van der Rest, M.
J. Biol. Chem. 262, 17724-17727, 1987
A;Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of pepsin A;Reference number: S22254; MUID:88087065; PMID:3121603

A;Molecule type: protein

A;Molecule type: protein A;Residues: 'X',1333','Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517 A;Residues: 'X',1333','Q',1335-1347;1914-1928;2504,'X',2506,'X',2508-2511,'X',2513-2517 A;Cross-references: UNIPARC:UPI0000173C41; UNIPARC:UPI0000173C42; UNIPARC:UPI0000173C43

A; Accession: S23814

45	44	43	42	41	40	9	38	37	36	35 5	34.	33	32 .	31	30
150.5	151	151.5	152	153.5	154	157.5	160	161	162	162.5	162.5	163	163.5	164	165
7.0	7.0	7.0	7.1	7.1	7.1	7.3	7.4	7.5	7.5	7.5	7.5	7.6	7.6	7.6	7.7
1170	1914	1807	2477	2019	2265	1020	1907	1178	2813	2386	933	4135	1170	3566	1163
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803308	T42635	JC6319	·S14428	JQ1322	FNBO	A29355	S50893	S44142	UHWV	FNHU	A31930	T42629	I45914	A40701	156126
cell surface glyco	tenascin Y precurs	integrin beta-4 ch	fibronectin precur	tenascin precursor	fibronectin - bovi	fibronectin - chic	protein-tyrosine-p	VLA-2 protein homo	von Willebrand fac	fibronectin precur	cytotactin - chick	tenascin-X - bovin	integrin alpha 2 s	tenascin-X precurs	lymphocyte fuction

ALIGNMENTS

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F;332-414/Domain: fibronectin type III repeat homology FN38>
F;437-601/Domain: von Willebrand factor type A repeat homology
F;629-1178/Domain: IIIC #status predicted <IIIC>
F;630-711/Domain: fibronectin type III repeat homology FN3C>
F;721-802/Domain: fibronectin type III repeat homology FN3D>
F;812-895/Domain: fibronectin type III repeat homology FN3F>
F;905-966/Domain: fibronectin type III repeat homology FN3F>
F;905-1076/Domain: fibronectin type III repeat homology FN3F>
FN3F>
FN3F-1076/Domain: fibronectin type III repeat homology FN3F>
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F;2509-2750/Domain:
F;2751-2902/Domain:
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F;24-105/Domain: fibronectin type III repeat homology <FN3A>
F;337-301/Domain: von Willebrand factor type A repeat homology
F;332-425/Domain: IIIB #status predicted <IIIB>
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Biochim. Biophys. Acta 1171, 97-9
A;Title: The two splice variants
A;Reference number: S28811; MUID:
A;Accession: S28811
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F;2119-2199/Domain:
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A;Cross-references: UNIPARC:UPI0000173C46; EMBL:X67327
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A;Cross-references: UNIPARC:UPI0000173C44; UNIPARC:UPI0000173C45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary
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Best Local
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LRIEQELAAIRKKSYVPAKNMVFSDVTSDSFKVSWSAAGSEEKSYLIKYKV--AIGGDEF
                                                                                                                                                   KEPAIKLRDADVEIFAVGVKDAVRTELEAIASPPAETHVYTVEDFDAFQRISFELTQSVC
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in: fibromectin type III repeat homology <FN3J>
in: fibromectin type III repeat homology <FN3J>
in: fibromectin type III repeat homology <FN3K>
in: fibromectin type III repeat homology <FN3L>
in: fibromectin type III repeat homology <FN3M>
in: fibromectin type III repeat homology <FN3M>
in: fibromectin type III repeat homology <FN3P>
in: von Willebrand factor type A repeat homology <WN3P>
in: IXP, homologous to NC4 domain of type IX collage
in: collagenous COL2 #status predicted <COL2>
on: cell attachment (R-G-D) motif
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31.1%;
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A,Molecule type: mRNA
A,Molecule type: mRNA
A,Residues: 'EFR',372-517,'DV',520-540,'W',542-1255 <RES>
A,Cross-references: UNIPARC:UPI000016B3AC; GB:S51236; NID:g262308; PIDN:AAB24637.1;
A,Cross-references: UNIPARC:UPI000016B3AC; GB:S51236; N.P.; Glanville, R.W.; Burgeson,
R,Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgeson,
J. Biol. Chem. 264, 3822-3826, 1989
J. Biol. Chem. 264, 3822-3826, 1989
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A;Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion prot A;Reference number: I56328, MUID:93107742; PMID:1469284
A;Accession: I56328
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A;Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the A;Reference number: S16316; MUID:91334380; PMID:1871109
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A54849
                                                                                                                                          Hum. Mol. Genet. 2, 273-278, 1993
A; Title: The carboxyl-terminal half of type
A; Reference number: 148103; MUID:93271985; I
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A;Molecule type: protein
A;Residues: 'A',1240-1246,'G',1248-1250,'XE',1253-1255,'Q',1257,'E';2032,'C',2034-2041;'
A;Cross-references: UNIPARC:UPI000017A13A; UNIPARC:UPI000017A13B; UNIPARC:UPI000017A13C;
A;Cross-references: UNIPARC:UPI000017A13A; UNIPARC:UPI000017A13C;
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A;Residues: 815-892, E',894-1439 <PAR>
A;Residues: 815-892, E',894-1439 <PAR>
A;Cross-references: Unitable Control of the Control of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA, A;Molecule type: mRNA, A;AO-A;AO, A;AO, A;A
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A;Title: Molecular cloning and characterization of type
A;Reference number: PH0844; MUID:92231902; PMID:1567409
A;Accession: PH0844
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A;Residues: 1-2944 <CHR>
A;Cross-references: UNIPROT:Q02388; UNIPARC:UPI000017A138; GB:L02870; NID:g987124;
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                                                                     A; Reference number: A; Accession: I84686
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A;Reference number: A30296; MUID:89139437; PMID:2537292
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A;Status: preliminary; translated from
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A;Cross-references: GDB:128750;
A;Map position: 3p21.3-3p21.3
A;Note: defects in this gene ca
A;Note: there are 118 introns
C;Complex: type VII collagen is
C;Function:
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F;36-201/Domain: von Willebrand factor type A repeat homology <WWA1>
F;331-318/Domain: fibronectin type III repeat homology <FNI>
F;327-413/Domain: fibronectin type III repeat homology <FN2>
F;414-502/Domain: fibronectin type III repeat homology <FN3>
F;508-593/Domain: fibronectin type III repeat homology <FN4>
F;598-683/Domain: fibronectin type III repeat homology <FN4>
F;598-683/Domain: fibronectin type III repeat homology <FN5>
F;686-771/Domain: fibronectin type III repeat homology <FN8>
F;76-862/Domain: fibronectin type III repeat homology <FN9>
F;76-862/Domain: fibronectin type III repeat homology <FN9>
F;776-862/Domain: fibronectin type III repeat homology <FN9>
F;76-862/Domain: fibronectin type III repeat homology <FN9>
F;776-862/Domain: fibronectin type III repeat homology <FN9>
F;76-862/Domain: fibronectin type III
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A;Cross-references: UNIPARC:UPIO00016A724; GB:L06862; NID:g388713; PIDN:AAA89196.1; R;Christiano, A.M.; Ryynaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A;Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly ---> Ser
A;Reference number: A55255; MUID:94224777; PMID:8170945
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Best Local S
Matches 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene: GDB:COL7A1; EBR1; EBD1; EB;Cross-references: GDB:128750; OMIM:120120
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                                         272
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                                                                                                                 RDLVLSEPSSQSLRVQWTAASGPVTGYKVQYTPLTGLGQPLPSERQEVNVPAGETSVRLR
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31.0%;
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F;29-1857/Froduct: collagen alpha I(XIV) chain, short form #status predicted F;29-110/Domain: fibronectin type III repeat homology <FN3A>
F;156-320/Domain: von Willebrand factor type A repeat homology <FN3B>
F;352-433/Domain: fibronectin type III repeat homology <FN3B>
F;442-525/Domain: fibronectin type III repeat homology <FN3D>
F;534-614/Domain: fibronectin type III repeat homology <FN3D>
F;623-707/Domain: fibronectin type III repeat homology <FN3B>
F;741-823/Domain: fibronectin type III repeat homology <FN3B>
F;741-823/Domain: fibronectin type III repeat homology <FN3G>
F;832-914/Domain: fibronectin type III repeat homology <FN3G>
F;832-914/Domain: fibronectin type III repeat homology <FN3H>
F;922-1009/Domain: fibronectin type III repeat homology <FN3H>
F;1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>
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A; Residues: 1-1857 < WABS
A; Cross-references: UNIPARC: UPI000017123C; EMB
A; Note: the nucleotide sequence was submitted
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A;Title: Complete primary structure of chicken collagen
A;Reference number: S31211; MUID:93185668; PMID:8444186
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117; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRTVCSRVEEQEKEIKGTIAASLGAPTDLVTSDITARGFRVSW----
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28.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 380.5; DB 2
Pred. No. 9.1e-19;
3; Mismatches 158
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F;442-255/Domain: fibronectin type III repeat homology <FN3C>
F;534-614/Domain: fibronectin type III repeat homology <FN3C>
F;623-707/Domain: fibronectin type III repeat homology <FN3E>
F;741-823/Domain: fibronectin type III repeat homology <FN3F>
F;832-914/Domain: fibronectin type III repeat homology <FN3G>
F;832-914/Domain: fibronectin type III repeat homology <FN3G>
F;922-1009/Domain: fibronectin type III repeat homology <FN3G>
F;1040-1205/Domain: von Willebrand factor type A repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;1-20/Domain: signal sequence #status predicted <SIG>
F;29-1088/Product: collagen alpha I(XIV) chain, long form #status predicted <MAT>
F;29-110/Domain: fibronectin type III repeat homology <FNIJA>
F;156-320/Domain: von Willebrand factor type A repeat homology <VWA1>
F;352-433/Domain: fibronectin type III repeat homology <FNIJB>
F;352-433/Domain: fibronectin type III repeat homology <FNIJB>
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A;Residues: 1-416;1460-1811,1843-1888 <WAE>
A;Cross-references: UNIPARC:UPI00001773F4; UNIPARC:UPI00001773F5; EMBL:X70793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collagen alpha 1(XIV) chain precursor,
C;Species: Gallus gallus (chicken)
C;Date: 11-Mar-1998 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein;
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                                               EAQRVEVPAGRNCTTLQ--GLAPGTAYLVTVTAAFRSGRESALSAKACT 394
                                                                                                                                             VRLLRPQILRVRTRPEEAGPERIVISHARPRSLRVSWAPALGSAAALGYHVQFGPLRGG-
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AADEKEIKIGEASTELELDGLLPNTEYTVTVYAMFGEEASDPLTGQETT
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                                                                                                                                                                                               --PTRGGQPEEVVVDGSSSTAVLKNLMSLTEYQIAVFAIYSNAASEGLRGTETT
                                                                                                                                                                                                                                                                                                                                          ----ELRGSILDAM-RPQQLHATEITSSGFRLAWPPLLTADSG-----
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                                                                                               PMASDLKLYDVSHS---SMRAKWN---GVAGATGYMILYAPLTEGL
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A;Residues: 1472-1660 <APT>
A;Residues: UNIPARC:UPI0000006A2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1472-1659 <GOR1>
A;Cross-references: UNIPARC:UPI0000173C49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eur. J. Biochem. 207, 549-557, 1992
A;Title: Type XIV collagen is a variant of
A;Reference number: S22916; MUID:92339443;
A;Accession: S22916
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C;Keywords: alternative and a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA;
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A; Residues: 1551-1570; 1593-1599; 1639-1667 < GOR2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A45974
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                                                                                                                    Pred. No.
64; Mismatches
                                                                                                                                                              Score 369.5; DB 2
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PMID:1339349
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                                                                                                                                                                                          DB 2;
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N;Alternate names: undulin
N;Alternate names: undulin
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A45974; S30085; S222916; S17035; S20833
C;Accession: A45974; S30085; S222916; S17035; S20833
R;Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Canc
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F;236-317/Domain: fibronectin type III repeat homology <PW3A>
F;326-409/Domain: fibronectin type III repeat homology <PW3A>
F;418-498/Domain: fibronectin type III repeat homology <PW3C>
F;507-591/Domain: fibronectin type III repeat homology <PW3C>
F;507-591/Domain: fibronectin type III repeat homology <PW3D>
F;625-707/Domain: fibronectin type III repeat homology <PW3E>
F;716-998/Domain: fibronectin type III repeat homology <PW3F>
F;806-893/Domain: fibronectin type III repeat homology <PW3G>
F;924-1089/Domain: non-collagenous NC4 #status predicted <NC4>
F;1511-1552/Domain: non-collagenous NC2 #status predicted <NC2>
F;1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>
F;1511-155
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A;Residues: 286-494, 'Q', 496-834, 'A', 836-1119, 'KL', 1122-1402,1409-1439
A;Residues: UNIPARC:UPI0000173C48
R;Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsenmayer, T.F.; van der
Eur. J. Biochem. 201, 333-338, 1991
A;Title: Cloning of a cDNA for a new member of the class of fibril-ass
A;Reference number: S17035; MUID:92037585; PMID:1935930
A;Accession: S17035
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PFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVMVTDGG
                                                                                                                                                                                                                                                                                                                                                      PASAPRGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEF
                                                                                                                                                                                                                            PAIA---DIVILVDGSWSIGRFNFRLVRLFLENLVSRFNVGSEKTRVGLAQYSGDPRIEW
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R;Wei,
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A;Status: prelimina:
A;Molecule type: mRI
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A; Residues: 1-929 <WEI>
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A;Title: Monoclonal antibody MT2 identifies the urodele A;Reference number: I51027; MUID:95246925; PMID:7729585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type XII collagen alpha-1 chain - eastern newt (fragment)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
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Pred. No. 7.2e-12;
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grins, Von Willebrand factor,
A;Reference number: A33809; N
A;Accession: A33809
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-493 < KIS>
A;Cross-references: UNIPROT:F
                                                                                                                                                             cartilage matrix protein precursor - chicken
(;Species: Gallus gallus (chicken)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C;Accession: A33809; A26364
R;Kiss, I.; Deak, F.; Holloway Jr., R.G.; Delius, H.; Mebust, K.A.; Frimber
J. Biol. Chem. 264, 8126-8134, 1989
A;Title: Structure of the gene for cartilage matrix protein, a modular proteins, Von Willebrand factor, complement factors B and C2, and epidermal gr
A;Reference number: A33809; MUID:89255246; PMID:2542265
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F;165-246;Domain: fibronectin type III repeat homology <FN3
F;255-338/Domain: fibronectin type III repeat homology <FN3
F;257-338/Domain: fibronectin type III repeat homology <FN3
F;347-427/Domain: fibronectin type III repeat homology <FN3
F;347-632/Domain: fibronectin type III repeat homology <FN3
F;547-632/Domain: fibronectin type III repeat homology <FN3
F;547-632/Domain: fibronectin type III repeat homology <FN3
F;547-733/Domain: fibronectin type III repeat homology <FN3
F;641-723/Domain: fibronectin type III repeat homology <FN3
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J. Biol. Chem. 266, 17336-17332, 1991
A;Title: Undulin is a novel member of the fibronectin-tenascin
A;Reference number: A40970; MUID:91373351; PMID:1716629
A;Accession: A40970
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C; Date: 30-Jun-1992 #sequence
C; Accession: A40970
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A; Residues: 1-843 < JUS>
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25.7%;
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                                                                                                                                                                                                                                                                                            K.A.; Frimberger,
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epidermal growth
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UNIPROT: P05099;

UNIPARC: UPI000004F1EF; GB: X12346; GB: X12347;

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RESULT 10
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A; Residues: 78-493 <ARG>
A; Residues: 78-693 <ARG>
A; Cross-references: UNLPARC: UPI000004F1EE; GB: M14792; NID: 9211545; PIDN: AAA48695.1;
A; Cross-references: UNLPARC: UPI000004F1EE; GB: M14792; VOD Willebrand factor type A
C; Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A
F; 37-204/Domain: von Willebrand factor type A repeat homology <VWA1>
                                                                                                                                                                                   멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein A;Reference number: S66522; MUID:96270751; PMID:8665920 A;Accession: S66522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cartilage matrix protein precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 C;Accession: S66522
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A;Title: Structural features of cartilage matrix protein dedu. A;Reference number: A26364; MUID:87092429; PMID:3025875
A;Accession: A26364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-500 < ASZ>
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Best Local S
Matches 60
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Best Local S
Matches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;30-500/Product: cartilage matrix protein #status predicted <MAT>;43-210/Domain: von Willebrand factor type A repeat homology <VWA;231-266/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superfamily: cartilage matrix protein; EGF homology; 1-29/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225-260/Domain: EGF homology <EGF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 LVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVDVD 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 SSSVRQEFPLGQFKNKKDIKAAVKKMAYMEKGTMTGQALKYLVDSSFSIANGARPGVPKV 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKTCSACSGGSGSALDLVFLIDGSKSVRPENFELVKKFINQIVESLEVSEKQAQVGLVQY 316
                                                                                            IVVTDGRPQDSVRDVSERARASGIELFAIGLGRVDKATLRQIASEPQDEHVDYVE
                                                                                                                                      VWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFVD 194
                                                                                                                                                                                   KPEFPLRAHGSKASLLQAVRRIQPLSTGTMTGLALQFAITKALSDAEGGRARSPDISKVV
                                                                                                                                                                                                                              YTEFFFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGAR----PGVPKVL
                                                                                                                                                                                                                                                                                                                   PRG------DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRP
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                                                                                                                                                                                                                                                                           PRGHLCRTRPTDLVFVVDSSRSVRPVEFEKVKVFLSQVIESLDVGPNATRVGLVNYASTV
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34.3%;
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Pred. No. 4e-1
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                                                                                                                             Score 243.5;
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                  No. 9.3e-10;
smatches 75;
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A;Introns: 30/1; 236/1; 437/1; 638/1; 838/1
C;Superfamily: collagen VI
C;Superfamily: collagen VI
C;Superfamily: collagen VI
C;Keywords: alternative splicing; cell binding; coiled coil; connective tissue;
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-3137/Product: collagen alpha 3(VI) chain #status predicted <MAT>
F;26-3137/Product: collagen alpha 3(VI) chain #status predicted <MAT>
F;26-3137/Product: collagen alpha 3(VI) chain #status predicted <MAT>
F;26-202/Domain: von willebrand factor type A repeat homology <W002>
F;36-202/Domain: von willebrand factor type A repeat homology <W003>
F;442-607/Domain: von willebrand factor type A repeat homology <W005>
F;442-807/Domain: von willebrand factor type A repeat homology <W005>
F;1237-1400/Domain: von willebrand factor type A repeat homology <W007>
F;1439-1604/Domain: von willebrand factor type A repeat homology <W007>
F;1439-1604/Domain: von willebrand factor type A repeat homology <W008>
F;1639-1804/Domain: von willebrand factor type A repeat homology <W009>
F;1838-2010/Domain: von willebrand factor type A repeat homology <W009>
F;1838-2010/Domain: von willebrand factor type A repeat homology <W009>
F;2043-2378/Domain: collagenous #status predicted <CCL>
F;2045-2047/Region: cell attachment (R-G-D) motif
F;2153-2155/Region: cell attachment (R-G-D) motif
F;2159-2161/Region: cell attachment (R-G-D) motif
F;2623-2806/Domain: von willebrand factor type A repeat homology <W01>
F;2623-2806/Domain: von willebrand factor type A repeat homology <W01>
F;263-3039/Domain: platelet glycoprotein brobled <CCL>
F;263-3039/Domain: platelet glycoprotein Ib-like #status predicted <GPI>
F;201,2084,2436,2563,2581,2683,2867,2920,3003/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Bonaldo, P.; Colombatti, A.
J. Biol. Chem. 264, 20235-20239, 1989
A;Title: The carboxyl terminus of the chicken alpha3 chain.
A;Reference number: A32674, MUID:90062147; PMID:2584214
A;Accession: A32674
A;Molecule type: mRNA
A;Residues: 2151-2199;2792-3137 <BO2>
A;Cross-references: UNIPARC:UPI0000173C39; UNIPARC:UPI00001
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 224-2871 <BON>
A; Cross-references: UNIPARC: UPI0000173C38; GB: M24282
A; Cross-references: translated the codon TTC for residue
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A;Title: Structural and functional features of the alpha chain in A;Reference number: A34270; MUID:90212613; PMID:2322559
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A;Residues: 1-253;312-321;434-453;504-518;635-655;704-717;832-853 <DOL>
A;Cross-references: UNIPROT:P15989; UNIPARC:UPI0000173C31; UNIPARC:UPI0000173C32;
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J. Cell Biol. 111, 2197-2205, 1990
A;Title: Multiple forms of chicken alpha3(VI) collagen chain A;Reference number: A37797; MUID:91035630; PMID:1977751
A;Accession: A37797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                collagen alpha 3(VI) chain precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Aug-2004
C;Accession: A37797; A34270; A32674
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Best Local S
Matches 76
              117
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LVYAKEOLFAEASGAR---PGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGN 174
                                                                                LYDVVKALDVGGNDFRFALVQFSGNPHTEFQLNTYPSNQDVLSHIANMPYMGGGSKTGKG
                                                                                                                                                                                                                                                                                    LPWTA-LGLALSLRLALARSGAERGPPASAPR----GDLMFLLDSSASVSHYEFSRVREF
                                                                                                                                               VGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLA 116
                                                                                                                                                                                                              LPLAATLGLLLS---GFCSVGAQQ---QAAVRNVAVADITFLVDSSWSIGKEHFQLVREF
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                                                                                                                                                                                                                                                                                                                                                                               11.1%;
                                                                                                                                                                                                                                                                                                                                                   31;
                                                                                                                                                                                                                                                                                                                                                                                   Score 239; DB : Pred. No. 2e-08
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A;Reference number: A59140
A;Accession: A59140
A;Status: not compared with
A;Molecule type: mRNA
A;Residues: 1-3176 <CHU>
A;Cross-references: UNIPROT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cartilage matrix protein precursor - human
(7.Species: Homo sapiens (man)
(7.Species: Homo sapiens (man)
(7.Date: 12-Jul-1991 #sequence_revision 12-Jul-1991 #text_change 09-Jul-2004 ·
(7.Accession: A37979; B37979
(7.Accession: A37979; B37979
(8.Jenkins, R.N.; Osborne-Lawrence, S.L.; Sinclair, A.K.; Eddy Jr., R.L.; Byers, M.G.; Sh
J. Biol. Chem. 265, 19624-19631, 1990
A;Title: Structure and chromosomal location of the human gene encoding cartilage matrix
A;Reference number: A37979; MUID:91060568; PMID:2246248
A;Reference number: A37979; MUID:91060568; PMID:2246248
A;Residues: 1-496 < JEN>
A;Residues: 1-496 < JEN>
A;Cross-references: UNIFROT:P21941; UNIFARC:UPI000004F1ED; GB:J05867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: GDB:CRTM
A;Cross-references: GDB:127280; OMIM:115437
A;Map position: 1p35-1p35
A;Introns: 32/1; 147/3; 222/1; 264/1; 403/1; 454/1;
C;Complex: homotrimer
C;Superfamily: cartilage matrix protein; EGF homolog
C;Keywords: glycoprotein; homotrimer
                                                                                                                                                                                                     collagen alpha 3(VI) chain precursor [validated] - N;Contains: collagen alpha 3(VI) chain, splice form C;Species: Homo sapiens (man) C;Date: 21-Nov-1993 #seguence revision 12-Nov-1999 C;Accession: A59140; S13679; $24465; A57083; $28776 R;Chu, M.L.
                                                                                                                                                                                    submitted to GenBank,
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Best Local S
Matches 62
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[1-22/Domain: signal sequence #status predicted <SIG>
[23-496/Product: cartilage matrix protein #status predicted <MAT>
;39-206/Domain: von Willebrand factor type A repeat homology <VWA
;227-262/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273-437/Domain: von Willebrand factor type A repeat homology <VWA2>76,344/Binding site: carbohydrate (Asn) (covalent) #status predicte 221-238,234-247,249-262/Disulfide bonds: #status predicted
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                                                                                                    Status: not compared with conceptual
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PMQELKDLGVTVFIVSTGRGNFLELSAAASAP-AEKHLHFVDVDDLHIIVQELRGSI 209
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                    UNIPROT: P12111;
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                                                                                                                                                                                                                                        revision 12-Nov-1999 #text_change 16-Aug-2004
524465; A57083; S28776; S00245; C31952; C29848;
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Pred. No. 4.7e-09;
7; Mismatches 87
                    UNIPARC: UPI0000126D4F;
                                                                                                       translation
                                                                                                                                                                                                                                                                                                                           form
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                    GB:X52022; NID:G3127925;
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A; ROUTE Type: mRNA
A; Molecule type: mRNA
A; Residues: 'MRAWIFFLLCLAGRALAA', 3102-3176
A; Residues: 'MRAWIFFLCLAGRALAA', 3102-3176
A; Residues: UNIPARC: UPI0000173C30
                                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Residues: 'SAIAGVAGVG'
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A;Residues: 2038-2373 <CH4>
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A; Residues: 574-5
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                                                                                                       A;Accession:
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A;Residues: 574-585;965-973,'X',975-976;1306-1325;1361-1377;1381-1401;1473-1506,'X',150-1962,'X',1564-1965;2018-2037;2374-2410;2445-2459;2466-2469,'X',2471-2471;2504-2508,'X',A;70-1962,'X',1504-1965;2018-2037;2374-2410;2445-2459;2466-2469,'X',2471-2471;2504-2508,'X',A;70-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1504-1962,'X',1
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A;Residues: 2092-2151 *WEI>
A;Residues: 2092-2151 *WEI>
A;Residues: 2092-2151 *WEI>
A;Residues: 2092-2151 *WEI>
A;Cross-references: UNIPARC:UPI000016A720; GB:M27449; NID:g291919; PIDN:AAA52057.1;
A;Note: part of this sequence was determined by protein sequencing
R;Jander, R.; Rautenberg, J.; Glanville, R.W.
Bur. J. Biochem. 133, 39-46, 1983
Bur. J. Biochem. 133, 39-46, 1983
A;Title: Further characterization of the three polypeptide chains of bovine and huma
A;Reference number: $26506; MUID:83209648; PMID:6852033
A;Accession: $26510
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Bir. J. Biochem. 168, 309-317, 1987

A; Title: Characterization of three constituent chains of A; Paference number: S00126; MUID:88029444; PMID:3665927
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 32-126, 'AK', 129-136, 'L', 138-236 <ZA2>
A; Residues: 32-126, 'AK', 129-136, 'L', 138-236 <ZA2>
A; Cross-references: UNIPARC: UPI0000173C28; GB:S49432; NID:g260296; PIDN:AAB24261.1; PID
A; Cross-references: UNIPARC: UPI0000173C28; PIDN:AAB24261.1; PIDU:AAB24261.1; PIDU:AA
                                                                                                                                                                                                                                               A;Cross-references: UNIPARC:UPI0000173C2F
A;Note: this sequence cannot be reliably placed and probably
R;Mayer, U; Poeschl, E; Nischt, R; Specks, U; Pan, T.C.;
Eur. J. Biochem. 225, 573-580, 1994
A;Title: Recombinant expression and properties of the Kunitz-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: UNIPARC:UPI0000173C2E; GB:J04211; GB:M20778
A; Cross-references: UNIPARC:UPI0000173C2E; GB:J04211; GB:M20778
A; Note: parts of this sequence were determined by protein sequencing
A; Note: parts of this sequence were determined by protein sequencing
A; Note: parts of this sequence were determined by protein sequencing
A; Walter M. G.; Passage, E.; Van Cong, N.; Pribula-Conway, I
Am. J. Hum. Genet. 42, 435-445, 1988
A; Title: Cloning and chromosomal localization of human genes encoding
A; Reference number: A29848; MUID:88161046; PMID:3348212
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J. Biol. Chem. 263, 18601-18606, 1988
A;Title: Amino acid sequence of the triple-helical domain
A;Reference number: A31952; MUID:89066644; PMID:3198591
A;Accession: C31952
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A;Residues: 2024-2046;2092-2156,'R';2203-2208,'X',2210-2211,'X',2213-2227;2228-2251;231
A;Cross-references: UNIPARC:UPI000016A705; UNIPARC:UPI0000173C29; UNIPARC:UPI0000173C2A
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A;Residues: 310-328 <ZAN>
A;Cross-references: UNIPARC:UPI0000173C28
                                                                                                                                                                                A; Title: Recombinant expression and properties of the Kunitz-type A; Reference number: S48709; MUID:95045506; PMID:7525281
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A;Cross-references: UNIPARC:UPI0000173C14; EMBL:X52022; NID:g3127925
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EMBO J. 9, 385-393, 1990
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File2)Domain: signal sequence #status predicted <MATTIP Fig. 6-176/Product: collagen alpha 3(VI) chain #status predicted <AMTIP Fig. 6-207/Domain: anino-terminal nonhelical #status predicted <AMTIP Fig. 6-207/Domain: anino-terminal nonhelical #status predicted <AMTIP Fig. 6-307/Domain: von Willebrand factor type A repeat homology <WM02-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW02-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW03-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW03-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW03-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW03-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW03-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW03-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW03-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW03-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW03-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW03-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW03-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW03-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW03-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW03-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW03-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW03-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW03-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW03-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW03-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW13-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW13-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW13-Fig. 7-209/Domain: von Willebrand factor type A repeat homology <WW13-Fig. 7-209/Domain: von Wille
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A;Cross-references: GDB:119066; OMIM:120250
A;Cross-references: GDB:119066; OMIM:120250
A;Cross-references: GDB:119066; OMIM:120250
A;Cross-references: GDB:119066; OMIM:120250
C;Complex: type VI collagen is a heterotrimer of one alpha 1(VI) chain (see PIR:CGHUIA)
Sociations among trimer amino- and carboxyl-terminal domains (with disulfide bonds).
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A;Reference number: A52812; PDB:IKNT
A;Contents: annotation; X-ray crystallography, 1.6 angstroms, residues 3106-3160
A;Note: engineered sequence expressed in Saccharomyces cerevisiae strain mt-663
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit sines are 5-hydroxylated and subsequently O-glycosylated.
C;Comment: The fibronectin type III repeat homology domain may be released during proce
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C; Keywords: alternative splicing; blocked amino end; cell binding; coiled
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Best Local
                                                                                                                                  159
                                                                                                                                                                                                     152
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                                                                                                                                                                                                                                                                                                                                            94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                               DAMRPQQLHATEITSSGFRLAWPPLLTADSGYYVLELVPSAQPGAARRQQLPGNATDWIW
                                                                                                                                  ALPSAELKSADVNVFAIGVEDADEGALKEIASEPLNMHMFNLENFTSLHDIVGNLVSCVH
                                                                                                                                                                                                  GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL-HFVDVDDLHIIVQELRGSIL
                                                                                                                                                                                                                                                                                                                                 GEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGAR--PGVPKVLVWVTDGGSSDPV
                                                                                                                                                                                                                                                                                                                                                                                                        DIIFLVDSSWTIGEEHFOLVREFLYDVVKSLAVGENDFHFALVOFNGNPHTEFLLNTYRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS
SSVSPERAGDTETLKD--
                                                                                                                                                                                                                                                                         KQEVLSHISNMSYIGGTNQTGKGLEYIMQSHLTKAAGSRAGDGVPQVIVVLTDGHSKDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 225.5; DB 2;
Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 143;
-ITAQDSADIIFLID--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51;
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                                                                                                                                                               Query Match
Best Local
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R;Kern, A.; Briesewitz, R.; Bank, I.; Marcantonio, E.E.
J. Biol. Chem. 269, 22811-22816, 1994
A;Title: The role of the I domain in ligand binding of the human integrin alpha-1beta-1
A;Reference number: A55348; MUID:94357930; PMID:7521332
A;Accession: A55348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Gallus gallus (chicken)
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C;Accession: A55348
C;Accession: A55348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein DKFZp434J065.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #te
C;Accession: T46488
                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-272 <KER>
A;Residues: 1-272 <KER>
A;Cross-references: UNIPROT:O42094; UNIPARC:UPI000017A14E; GB:U10114
F;55-230/Domain: von Willebrand factor type A repeat homology <VWA2>
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A;Experimental source: adult testis; clone DKFZp434J065
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z23035
A; Accession: T46488
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A; Residues: 1-741 < AAA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 DIMFILDSSASVSHYEFSRVREFVGQLVAPLPIGTGALRASLVHVGSRPYTEFPFGQHSS
                                                                                                      34 DLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS 93
                                                                                                                                                                                                                                                                                Similarity
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DIVIVEDGSNSI--YPWESVTAFLNSLLRNMDIGPQQTQVGIVQYGQTVVHEFYLNTYST
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                                                                                                                                                                                                                  9.7%; Score 209; DB 2;
33.6%; Pred. No. 1.2e-07;
ative 31; Mismatches 85
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Pred. No. 7.1e-08;
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SMART; SM00327; VWA; 1
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PROSITE; PS50234; VWFF
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Von Willebrand factor A domain-related protein (Mus musculus 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriched library, clone:5031410123 product:VON WILLERDANT --
RELATED PROTEIN homolog).
Mammary tumor metastatized to lung. Tumor arose spontaneously; MEDLINE-22380257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D. Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.
                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
Muroidea; Muridae;
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Euarchontoglires;
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lires; Rodentia;
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RA RA Whiting M. Madan A., Young A.C., Shevchenko Y., Boutfard G.G., RA Bodak S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Toubhman J.W., Green E.D., Dickson M.C., RA Bouterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15.000 ferror and mouse cDNA sequences.";

1. Proc. Natl. Acad. Sci ""-"
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RC STRAING STRA
                                                                                                                                                                     STRAIN-C57BL/GJ; TISSUE-Ovary and uterus;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata Konno H., Okazaki Y., Muramatsu N., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDN prepare full-length cDNA libraries for rapid discovery of Genome Res. 10:1617-1630(2000).
NUCLEOTIDE SEQUENCE.
STRAIN-C57BL/60; TISSUE-Ovary and uterus;
MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based c 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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STRAIN=C57BL/6J; TISSUE=Ovary and
The FANTOM Consortium,
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; DOI=10.1016/S0076-6879(99)03004-9;
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A Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
A Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
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A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
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A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
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A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.
A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS50234; VWFA; 1
SEQUENCE 415 AA; 44709
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GO; GO:0005615; C:extracellular space; TAS InterPro; IPR003961; FN III.
InterPro; IPR00395; VWF A.
Pfam; PF00041; fn3; 2.
Pfam; PF000041; fn3; 2.
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STRAIN=FVB/N; TISSUE=
Director MGC Project;
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BL; AK077240; BAC36703.1; -; mRNA.
BL; BC036166; AAH36166.1; -; mRNA.
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TRPEEAGPERIVISHARPRSLRVSWAPALGSAAALGYHVQFGPLRGGEAQRVEVPAGRNC
                                                                                                                                                                                                                              KEQLFAEEAGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTIFIVSTGRGNLLELLA
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1657.5;
Pred. No. 3.8e
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rabe Y., Tagami P
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Best Local :
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SWART; SM00060; FN3; 2.
SMART; SM00327; VWA; 1.
PROSITE; PS50653; FN3; 2.
PROSITE; PS50234; VWFA; 1.
SEQUENCE 415 AA; 44737 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22057805; PubMed=12062410; DOI=10.1016/S0014-5793(02)02579-6; Fitzgerald J., Ting S.T., Bateman J.F.; WARP a new member of the von Willebrand factor A-domain superfamily of extracellular matrix proteins."; FEBS Lett. 517:61-66(2002).

EMBL; AY030094; AAX38350.1; -; mRNA.
HISSP; P18614; 1MHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q923K3_MOUSE PRELIMINARY; PRT; 415 AA.
Q923K3;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation updat
Von Willebrand factor A-related protein.
Name='Wwal; Synonyms=4932416AllRik, Warp;
The musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata
Mammalia; Eutheria; Euarchontoglires;
Muroidea; Muridae; Murinae; Mus.
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Ensembl; ENSMUSGO0000042116; Mus
MGI; MGI:2179729; 4932416A11Rik.
MGI; MGI:2179729; Vwal.
GG; GO:0005615; C:extracellular &
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                                                            GYYVLELVPSAQPGAARRQQLPGNATDWIWAGLDPDTDYDVALVPESNVRLLRPQILRVR
                                                                                                          AASAPAEKHLHFVDVDDLHIIVQELRGSILDAMRPQQLHATEITSSGFRLAWPPLLTADS
                                                                                                                                            KEQLFAEASGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSA
                                                                                                                                                                                            VAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYA
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                                               GYYVLELVPSGKLATTRROOLPGNATSWTWTDLDPDTDYEVSLLPESNVHLLRPQHVRVR
                                                                                              AASAPAEKHLHFVDVDDLPIIARELRGSITDAMQPQQLHASEVLSSGFRLSWPPLLTADS
TLQEEAGPERIVISHARPRSLRVSWAPALGPDSALGYHVQLGPLQGGSLERVEVPAGQNS
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                                                                                                                                                                                                                                                                                                         76.8%;
77.5%;
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Pred. No. 7.16
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A Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

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Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

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Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

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A Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

A Blake J., Boilt C., Fletcher C., Fujita M., Gariboldi M.,

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A Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,

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A Horashia H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

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A Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

A Hayashiaki A., Y., Soshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Q8C0Q7_MOUSE
Q8C0Q7;
01-MAR-2003
                                                                                                                        Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., "Normalization and subtraction of cap-trapper-selected cDNAs prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
   NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TIS
MEDLINE=20530913; Pu
                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=20499374; PubMed=11042159;
                                                                                                                                                                                                                                                                                                                                                                                                         the RIKEN Genome Exploration Research "Analysis of the mouse transcriptome 60,700 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Testis; The FANTOM Consortium,
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MEDLINE=99279253; PubMed=10349636; DOI=10.10
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
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Mammalia; Eutheria;
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004 (TrEMBLrel. 26, Last annotation update)
001 (TremBLrel. 26, Last annotation update)
0101 adult male testis cDNA, RIKEN full-length enriched
0101 clone:4932416A11 product:VON WILLEBRAND FACTOR A-RELATED
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TISSUE=Testis; pubMed=11076861;
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   DOI=10.1101/gr.152600;
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based o
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lires; Rodentia; Sciurognathi;
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A Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

A Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,

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Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.

A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

Zasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

B Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

Submitted (JUL-2001) to the EmBL/GenBank/DDBJ databases.

EMBL; AKO30019; BAC26739.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50853; FN3; 2. PROSITE; PS50234; VWFA; 1 SEQUENCE 415 AA; 44681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00453; VWFADOMAIN SMART; SM00060; FN3; 2. SMART; SM00327; VWA; 1.
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MGI; MGI:2179729; 4932416A11R1k
MGI; MGI:2179729; Vwal.
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                                                                                                                                                                                                                                                                      AASAPAEKHLHFVDVDDLHIIVQELRGSILDAMRPQQLHATEITSSGFRLAWPPLLTADS
                                                                                                                                                                                                                                                                                                                                                KEQLFAEASGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSA
                                                                                                                                                                                                                                                                                                                                                                                                                                   VAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MLPWTALGLALSLRLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQL
                                    TTLQGLAPGTAYLVTVTAAFRSGRESALSAKACTPDGPRPRPRPVPRAPTPGTASREP
                                                                                                                     TRPEEAGPERIVISHARPRSLRVSWAPALGSAAALGYHVQFGPLRGGEAQRVEVPAGRNC
                                                                                                                                                           GYYVLELVPSGKLATTRRQQLPGNATSWTWTDLDPDTDYEVSLLPESNVHLLRPQHVRVR
                                                                                                                                                                                                                                                                                                                             KEQLFAEEAGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGATIFIVSTGRGNLLELLA
                                                                                                                                                                                                                                                                                                                                                                                                              VATMSFGPGALRASLVHVGSQPHTEFTFDQYSSGQAIQDAIRVAPQRMGDTNTGLALAYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MLFWTAFSMALSLRLALARSSIERGSTASDPQGDLLFLLDSSASVSHYEFSRVREFVGQL
                                                                              TLQEEAGPERIVISHARPRSLRVSWAPALGPDSALGYHVQLGPLQGGSLERVEVPAGQNS
                                                                                                                                                                                                                                            AASAPAEKHLHFVDVDDLPIIARELRGSITDAMQPQQLHASEVLSSGFRLSWPPLLTADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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44681 MW;
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77.5%;
VTVTAAFRSGRORALSAKACTASGARTR
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Pred. No. 7.1e
31; Mismatches
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AS Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

AR Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

AR Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

AR Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

AR Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

AR Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

AR Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

AR Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

AR Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

AR Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

AR Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

AR Brownstein M.J., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

AR Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

AR Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

AR Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

AR Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

AR Richards S., Worley K.C., Hale S., Garcia B.J., Lu X., Gibbs R.A.,

AR Hillian D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

AR Richards S., Worley K.C., Hale S., Garcia B.J., Lu X., Gibbs R.A.,

AR Hillian D.K., Worley K.C., Hale S., Garcia B.J., Lu X., Gibbs R.A.,

AR Richards S., Worley K.C., Hale S., Garcia B.J., Lu X., Gibbs R.A.,

AR Richards S., Worley K.C., Hale S., Garcia B.J., Not Septen S.J.,

AR Richards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

AR Richards S., Worley R.W., Touchman J.W., Green E.D., Dickson M.C.,

AR Richards S., Worley R.W., Touchman J.W., Green E.D., Dickson M.C.,

AR Richards S., Schein J.E., Jones S.J.M., Marra M.A.;

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Brown M. R. S., Sander S., Worley R.W., Touchman J. W., Green E.D., Dickson M.A.;

Brown R. S., Sander S., World R. W., World R. W., World
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local (
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Von Willebrand factor A domain-related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00060; FN3; 2.
SMART; SM00327; VWA; 1.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BC081983, AAH81983.1; -; mRNA.
InterPro; IPR003961; FN III.
InterPro; IPR002035; VWF_A.
Pfam; PF00041; En3; 2.
Pfam; PF00092; VWA; 1.
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                                                                                                                                                                            VAPLPIGTGALRASIVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYA
                                        KEQLFAEASGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSA
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77.8%;
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31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1643.5;
Pred. No. 3.56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B3A0A0268DB06D4E CRC64;
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3.5e-104;
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RESULT 6
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Ram G.M., Hong L.,
RA Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Schein J.E., Jones S.J.M., Marra M.A.;
Tand mouse cDNA sequences.";
The Description of Mark Market Market Huller Huller
   Matches
                              Query Match
Best Local Similarity
                                                                                                                       Pfam; PF00041; fn3; 2.

SMART; SM00060; FN3; 1.

PROSITE; PS50853; FN3; 2.

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SEQUENCE 281 AA; 29628 N
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13-SEP-2005
13-SEP-2005
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Q7L5D7;
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(TrEMBLrel.
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   Conservative
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                                                                                                                                 29628 MW;
                              60.1%;
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Score 1295.5;
Pred. No. 1.4e
0; Mismatches
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                              1295.5;
No. 1.4e
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   Indels
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Sciurognathi;

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RESULT 7
Q9H6J5 HUMAN
ID G9H6J5;
AC Q9H6J5;
DT 01-MAR-2001 (T)
DT 01-MAR-2001 (T)
DT 01-MAR-2001 (T)
DT 01-GT-2003 (T)
DT 01-MAR-2001 (T)
DR NUCLEOTIDE SEC
RA Watanabe K., F
RA Watana
RESULT 8
Q8VDV9_MOUSE F
ID Q8VDV9;
AC Q8VDV9;
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Best Local S
Matches 206
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Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS50853; FN3; 2.
SEQUENCE 233 AA; 24473 MW; 1
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Watanabe K., Kumagai A., Itakura
Suzuki Y., Obayashi M., Nishi T.,
Nakamura Y., Isogai T., Sugano S.
Submitted (AUG-2000) to the EMBL,
EMBL; AK025868; BAB15264.1; -; ml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Hypothetical protein FLJ22215.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                              366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                          LDPDTDYDVALVPESNVRLLRPQILRVRTR-------
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                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.1%;
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™ahi T., Shibahara T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1058.5; DB 2;
Pred. No. 1.8e-64;
0; Mismatches 0;
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                         PRT;
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ibahara T., Tanaka
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Manmary tumor metastatized to lung. Tumor arose spontaneously;

RX MEDLINE-22388257; PubMed-12477932; DOI-10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschuk S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Bosak S.S., Loquellano N.A., Beters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

RA Rahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Raha S., Schein J.S., Jones S.J.M., Wyers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

RT Tacch Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003961; FN_III. Pfam; PF00041; fn3; 2. SMART; SM00060; FN3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ensemb); ENSMUSG0000042116; Mus mus MGI; MGI:2179729; 4932416A11Rik.
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01-MAR-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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                      181
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                                                                                                                                     AALGYHVQFGPLRGGEAQRVEVPAGRNCTTLQGLAPGTAYLVTVTAAFRSGRESALSAKA
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                                                                CTPDGPRPRPRPVPRAPTPGTASREP
                                                                                                                                                                                                   LDPDTDYEVSLLPESNVHLLRPQHVRVRTLQEEAGPERIVISHARPRSLRVSWAPALGPD
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                      CTASGARTR --- APQSMRPEAGPREP
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73.3%;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                          Score 782.5; DB 2
Pred. No. 1.2e-45;
7; Mismatches 35
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A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
A Micaud S., Jaffe D., Fishers S., Lutfalla G., Dossat C., Segurens B.,
A Micaud S., Jaffe D., Fishers S., Lutfalla G., Dossat C., Segurens B.,
A Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
A Anthouard V., Jubin C., Cattelli V., Katinka M., Vacherie B.,
A Anthouard V., Jubin C., Cattelli V., Katinka M., Vacherie B.,
A Hindbard C., Skalli Z., Cattelli P., Coutanceau J.P., Gouzy J.,
A Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
A Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
A Kallis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
A Kallis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
A Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Mincher P., Lander E.S., Weisenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
hature 431:946-957 (2004).
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Best Local S
Matches 146
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome undetermined SCAF14659, whole genome sho
ORFNames=GSTENG00020556001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whi
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Q4SCD1;
13-SEP-2005 (Trembire). 3
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VTVTAAFRSGRESALSAKACTPDG
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                                                                                              TESGATSVRLSWGP-LQPQTVRDYYIEYSALPRGELRTATVDRTQNSTLLRRLQPGTTYL
                                                                                                                                                      SHARPRSLRVSWAPALGSAAALGYHVQFGPLRGGEAQRVEVPAGRNCTTLQGLAPGTAYL
                                                                                                                                                                                                                       SQYQRLVQPAASSTAKLTGLKPDTTYTVTLIPESNEHTFNALTTTTTKPEVLSPVVVTV
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55316 MW; C724FA399E0751FC
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Pred. No. 1.9e-38;
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1 CHICK S
COCA1 CHICK S
P13944; Q04509;
01-JAN-1990 (Rel
                                                                            MEDLINE=93042014; PubMed=1420368; DOI=10.1016/0
Trueb J., Trueb B.;
Trueb J., Trueb B.;
"The two splice variants of collagen XII share
Biochim. Biophys. Acta 1171:97-98(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                        to type J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamagata M., Yamada K.M., Yamada S.S., Shinom Nishida Y., Obara M., Kimata K.; "The complete primary structure of type XII comolecule with reiterated fibronectin type III factor A motifs, a domain homologous to a nonc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Last sequence update)
10-WAY-2005 (Rel. 47, Last annotation update)
Collagen alpha 1(XII) chain precursor (Fibrochimerin)
                                                                                                                                                                                                                                                                                                                                                                           "Type XII collagen: distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=White leghorn;
MEDLINE=92011862; Publ
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Eukaryota; Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                                                      Proc.
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Gordon M.K., Gerecke D.R., Dublet
"Type XII collagen. A large multio
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                                                                                                                                                                                                                                                                                                                                                                  CDNA
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                    Event=Alternative splicing; Named isoforms=2; Comment=The final tissue form of collagen XII may contain homotrimers of either isoform Long or isoform Short or any combination of isoform Long and isoform Short. Only isoform Long is a proteoglycan. Isoform Long has more restricted expression
                                                                                                                                                                                                                                                                                                                                                      Natl. Acad. Sci. U.S.A.
             is a proteoglycan. Isoform Long has mor
in embryonic tissue than isoform Short;
                                                                                                                                                                                                                                                                                                                                                                  cloning.";
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da K.M., Yamada S.S., Shinomura T., Tanaka
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; Galliformes; Phasianidae; Phasiani
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Pfam; PF00041; fn3; 17.

Pfam; PF00092; VWA; 4.

Pfam; PF00092; VWA; 4.

PRINTS; PR0045; VWFADOMAIN.

SMART; SM00000; FN3; 18.

SMART; SM00327; VWA; 4.

SMART; SM00327; VWA; 4.

PROSITE; PS50853; FN3; 18.

PROSITE; PS5034; VWFA; 4.

Alternative splicing; Cell adhesion; Collagen;

M Alternative splicing; Extracellular matrix; Glyc

M Direct protein sequencing; Extracellular matrix; Glyc

Hydroxylation; Repeat; Signal; Structural protein.
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EMBL; X61024; CAA43358.1; -; m
EMBL; M17375; AAA48718.1; -; m
EMBL; M015137; AAA48635.1; -; m
EMBL; X67327; CAA47744.1; -; m
PIR; A40020; A40020.
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InterPro; IPR003961; FN III.
InterPro; IPR003129; Laminin_G_TSP_N.
InterPro; IPR002035; VWF A.
Pfam; PF01391; Collagen; 4.
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DOMAIN: This sequence defines five distinct domains, two triple-helical domains (COL1 and COL2) and three nontriple-helical domains (NC1, NC2, and NC3).

PTM: The triple-helical tail is stabilized by disulfide bonds at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European Bioinformatics Institute. There are no restrictions as long as its content is in no way modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s Swiss-Prot entry is copyright. It is produced ween the Swiss Institute of Bioinformatics and European Bioinformatics Institute. There are I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the fibril-associated interrupted helices (FACIT) family.
SIMILARITY: Contains 18 fibronectin type-III SIMILARITY: Contains 1 TSP N-terminal (TSPN) SIMILARITY: Contains 4 VWFA domains.
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Oglycosylated; glycosaminoglycan of chondroitin-sulfate tsimilarity).
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Nonhelical region (NC2)
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VWFA 4.
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S (in Ref. 4).

E (in Ref. 2).

A (in Ref. 2).

F (in Ref. 2).

F (in Ref. 2).

AG (in Ref. 3).
                                                                                                                                                                     --VLRYRLVYRPLTGGERRQVTVSANERSTTLRNLI
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    817
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Q5VYK2_HUMAN PRELIMINARY;
AC Q5VYK2;
AC Q1-FEB-2005 (TrEMBLrel. 29, DT 01-FEB-2005 (TrEMBLrel. 31, alpha 1)
DE C01Lagen, type XII, alpha 1)
DE C01Lagen, type XIII, alpha 1, alpha 2, alpha 2, alpha 1, alpha 2, alpha 2, alpha 2, alpha 2, alpha 1, alpha 2, alph
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R GO; GO:0005737; C:cytoplasm; IEA.

R GO; GO:000578; C:extracellular matrix (sensu Metazoa); IEA.

R GO; GO:0005198; F:structural molecule activity; IEA.

R GO; GO:0005118; F:structural molecule activity; IEA.

R GO; GO:0006817; P:phosphate transport; IEA.

R GO; GO:0006817; P:phosphate transport; IEA.

R InterPro; IPR003129; Laminin G_TSP_N.

InterPro; IPR003129; Laminin G_TSP_N.

InterPro; IPR003129; Laminin G_TSP_N.

InterPro; IPR003129; Laminin G_TSP_N.

R InterPro; IPR00315; VWF A.

PFfam; PF0002035; VWF, A.

PFfam; PF000215; VWF, A.

PR PFfam; PF00041; fin3; 18.

PR PFAM; PF00041; Fin3; 18.

PR PFAM; SM001060; FSN; 18.

SWART; SM001060; TSN; 18.

PR PROSITE; PS00321; VWA; 4.

PR PROSITE; PS00334; VWFA; 4.

PR PROSITE; PS00321; VWA; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Sim
Matches 120;
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EMBL; AL080250; CAH19897.1; -; Genomic_DNA.
EMBL; AL096771; CAH19907.1; -; Genomic_DNA.
EMBL; AL096771; CAH71309.1; JOINED; Genomic_DNA.
EMBL; AL096771; CAH71309.1; JOINED; Genomic_DNA.
EMBL; AL096771; CAH19897.1; JOINED; Genomic_DNA.
EMBL; AL080250; CAH19907.1; JOINED; Genomic_DNA.
EMBL; AL354664; CAH19907.1; JOINED; Genomic_DNA.
EMBL; AL354664; CAH19907.1; JOINED; Genomic_DNA.
EMBL; AL096771; CAH19807.1; JOINED; Genomic_DNA.
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13-SEP-2005 (TrEMBIrel. 31, Last annotation update)
Collagen, type XII, alpha 1.
Name=COL12A1; ORFNames=RP1-238D15.1-003;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                  498
                                                                                                                                                                                                                                                                                                                              438
   210
                                                               558
                                                                                                                               152
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                                                                                                                                                                                                                                   SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
                                                                                                                                                                                                                                                                                                                                                                                          RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
                                                                                                                        GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGSI-
                                                                   RDPAIKLRNSDVEIFAVGVKDAVRSELEAIASPPAETHVFTVEDFDAFQRISFELTQSIC
                                                                                                                                                                                                  TKVEDIIEAINTFPYRGGSTNTGKAMTYVREKIFVPSKGSRSNVPKVMILITDGKSSDAF
                                                                                                                                                                                                                                                                                                                              KADIVFLVDGSYSIGIANFVKVRAFLEVLVKSFEISPNRVQISLVQYSRDPHTEFTLKKF
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   ---LDAMR-----PQQLHATEITSSGFRLAWPPLLTADSGYYVLELVPSAQPGAAR
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29,
31,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 424; DB
Pred. No. 9.4e-
68; Mismatches
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9.4e-20;
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Q5VYK1_HUMAN
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                                                                                                                                   EMBL; AL354664; CAH71310.1; -; Genomic_DNA.

EMBL; AL080750; CAI19898.1; -; Genomic_DNA.

EMBL; AL096771; CAI19908.1; -; Genomic_DNA.

EMBL; AL096771; CAF71310.1; JOINED; Genomic_DNA.

EMBL; AL096771; CAH71310.1; JOINED; Genomic_DNA.

EMBL; AL096771; CAH71310.1; JOINED; Genomic_DNA.

EMBL; AL080750; CAI19898.1; JOINED; Genomic_DNA.

EMBL; AL080750; CAI19908.1; JOINED; Genomic_DNA.

EMBL; AL096771; CAI19908.1; JOINED; Genomic_DNA.

EMBL; AL096771; CAI19898.1; JOINED; Genomic_DNA.

EMBL; AL096771; CAI19898.1; JOINED; Genomic_DNA.

EMBL; AL096771; CAI19998.1; JOINED; Genomic_DNA.
PRINTS; PRO0453; VWFADOMAIN.
SMART; SM00260; FN3; 18.
SMART; SM00210; TSPN; 1.
SMART; SM00327; VWA; 4.
PROSITE; PS50853; FN3; 18.
PROSITE; PS50834; VWFA; 4.
Collagen; Extracellular matri
SEQUENCE 3063 AA; 333147 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel 31, Last annotation update)
Collagen, type XII, alpha 1.
Name=COL12A; ORFNames=RP1-238D15.1-001;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                              Corby N.;
Submitted
                                                                                                              InterPro; IPR002035; VWF
Pfam; PF01391; Collagen;
Pfam; PF00041; fn3; 18.
Pfam; PF00092; VWA; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q5VYK1 HUMAN PRELIMINARY;
Q5VYK1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RQQL----PGNATDWIWAGLDPDTDYDVALVPESNVRLLRPQILRVRTRPEEAGPERIVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                (MAY-2005) to the EMBL/GenBank/DDBJ
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  Extracellular matrix; Repeat; Structural protein. 3063 AA; 333147 MW; EA38CAFECE8393D2 CRC64;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                Name=COL12A1;
Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; E
                                                                                                                Gerecke D.R., Olson P.F., Koch M., Knoll J.H.M., Taylor R.,
Hudson D.L., Champliaud M.-F., Olsen B.R., Burgeson R.E.;
"Complete primary structure of two splice variants of collagen XI
and assignment of alpha i(XII) collagen (COL12A1), alpha i(IX)
collagen (COL9A1), and alpha i(XIX) collagen (COL19A1) to human
chromosome 6q12-q13.";
Genomics 41:236-242(1997).
-i- FUNCTION: Type XII collagen interacts with type I collagen-
containing fibrils, the COL1 domain could be associated with
surface of the fibrils, and the COL2 and NC3 domains may be
localized in the perifibrillar matrix (By similarity).
-i- SUBUNIT: Trimer of identical chains each containing 190 kDa o
                                                                                                                                                                                                                                                                                                                                                                                     GOCA1 HUMAN STANDARD;

099715; 099716;

15-JUL-1998 (Rel. 36, Created)

15-JUL-1998 (Rel. 36, Last seq

10-MAY-2005 (Rel. 47, Last ann
                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE (ISOFORMS LONG AND SHORT),
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                          Collagen alpha 1(XII)
                                                                                                                                                                                                                                                              MEDLINE=97288521;    PubMed=9143499;    DOI=10.1006/geno.1997.4638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
            Name=Short;
                                              Event=Alternative splicing; Named isoforms=2; Comment=The final tissue form of collagen Inhomotrimers of either isoform Long or isoform combination of isoform Long and isoform Short;
                                                                                            ALTERNATIVE PRODUCTS:
                                                                                                       nontriple-helical sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        374
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                                             homotrimers of combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32
                        IsoId=Q99715-1;
  IsoId=Q99715-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDEVTVVEPASSTSVVLSSLKPETLYLVNVTAEYEDGFSIPLAGEETTEEVKGAPRNLKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSVIPEYFSGPGTPLTGNAATEE-VRGNPRDL-RVSDPTTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTVTAAFRSGRESALSAKACTPDGPRPRPRPVPRAPTPGTAS 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHARPRSLRVSWAPALGSAAALGYHVQFGPLRGGEAQRVEVPAGRNCTTLQGLAPGTAYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRIEQELAAIKKKAYVPPKDLSFSEVTSYGFKTNWSPAGENVFSYHI-----TYKEAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LDAMR-----PQQLHATEITSSGFRLAWPPLLTADSGYYVLELVPSAQPGAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RDPAIKLRNSDVEIFAVGVKDAVRSELEÄIÄSPPÄETHVFTVEDFDAFQRISFELTQSIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGSI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKVEDIIEAINTFPYRGGSTNTGKAMTYVREKIFVPSKGSRSNVPKVMILITDGKSSDAF
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                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Homin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.7%;
29.9%;
                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
chain precursor.
                       Sequence=Displayed;
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Pred. No. 1e-19;
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                                                                     XII may contain
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  InterPro; IPR008160; Collagen.
InterPro; IPR003961; FN III.
InterPro; IPR002035; VWF A.
Pfam; PP01391; Collagen; 4.
Pfam; PF00041; fn3; 18.
Pfam; PF00092; VWA; 4.
                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      + + +
                                                                                                                                                                                                                                                                                                                              Alternative splicing; Cell adhesion; Collagen; Direct protein sequencing; Extracellular matrix; G Hydroxylation; Repeat; Signal; Structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                      Hydroxylation; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00453; VWFADOMAIN. PROSITE; PS50853; FN3; 18. PROSITE; PS50234; VWFA; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U73778; AAC51244.1; -; EMBL; U73779; AAD40483.1; -; HSSP; P18614; 1MHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005595; C:collagen
GO; GO:0001501; P:skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGNC; HGNC:2188; COL12A1.
MIM; 120320; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ensembl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: O-glycosylation of isoform Long; glycosaminoglycan of chondroitin-sulfate type (By similarity).

SIMILARITY: Belongs to the fibril-associated collagens with interrupted helices (FACIT) family.

SIMILARITY: Contains 18 fibronectin type-III domains.

SIMILARITY: Contains 18 PN-terminal (TSPN) domain.

SIMILARITY: Contains 4 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               each end (By similarity).

PTM: Prolines at the third position unit (G-X-Y) are hydroxylated in son
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904
995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              its content is
                                  type XII; TAS.
development; TAS
                                                                     Fibronectin
Fibronectin
Fibronectin
                                                                                                                    Fibronectin
Fibronectin
Fibronectin
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            Nonhelical region
Triple-helical reg
                                  VWFA 4.
TSP N-terminal
                                                           Fibronectin
                                                                                                         Fibronectin
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+ TISSUE SPECIFICITY: Found in collagen I-containing tissues: isoform Short and isoform Long appear in amnion, chorion, shouscle, small intestine, and in cell culture of dermal fibroblasts, keratinocytes and endothelial cells. Only the in lung, placenta, kidney and a squamous cell chorion, skeletal Only the short poth

The triple-helical tail is stabilized by disulfide bonds at

he tripeptide repeating all of the chains (By

with

Swiss-Prot entry is copyright. It is produced through the Swiss Institute of Bioinformatics and the EM way modified There are no and thie restrictions EMBL statement outstation ç 18

a collaboration

Glycoprotein;

Fibronectin type-III Fibronect Fibronectin type-III Collagen alpha 1(XII) chain Fibronectin type-III 1. type-III type-III type-III type-III type-III type-III type-III region 9. 110. 111. 122. 133. 144. 115. 116. 117. (COL2) with 1

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Query Match
Best Local S
Matches 128
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REGION
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                                                                                                                                                                                                                          RDPAIKLRNSDVEIFAVGVKDAVRSELEAIASPPAETHVFTVEDFDAFQRISFELTQSIC
                                                                                                                                                                                                                                              GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGSI-
                                                                                                                                                                                                                                                                      TKVEDIIEAINTFPYRGGSTNTGKAMTYVREKIFVPSKGSRSNVPKVMILITDGKSSDAF
                                                                                                                                                                                                                                                                                         SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV
                                                                                                                                                                                                                                                                                                                    KADIVFLVDGSYSIGIANFVKVRAFLEVLVKSFEISPNRVQISLVQYSRDPHTEFTLKKF
                                                                                                                                                                                                                                                                                                                                SFKITWTQAPGRVLRCRIIYRPVAGGESREVTTPPNQRRRTLENLIPDTKYEVSVIPEYF
                                                                                                                                   VEPASSTSVVLSSLKPETLYLVNVTAEYEDGFSIPLAGEETTEEVKGAPRNLKVTDETTD
 TQEVTVRGDTTNTVLQGLKEGTQYALSVTALYASGAGDALFGEGTT
                    AORVEVPAGRNCTTLOGLAPGTAYLVTVTAAFRSGRESALSAKACT
                                           SGPGTPLTGNAATEEVRGNPRDLRVSDPTTSTMKLSWSGAPGKVKQ--YLVTYTPVAGGE
                                                               VRLLRPQILRVRTRPEEAGPERIVISHARPRSLRVSWAPALGSAAALGYHVQFGPLRGGE
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Apperfections.

Nonhelical region (NC1).

Cell attachment site (Potential).

Cell attachment site similarity).

Hydroxyproline (By similarity).
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                                                                                                                                                                                                PQQLHATEITSSGFRLAWPPL-------LTADSGYYV
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                                                                                                                                                                                                                                                                                                                                                                                                             MW;
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N-linked (GlcNAc...
N-linked (GlcNAc...
N-linked (GlcNAc...
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                                                                                                                                                                                                                                                                                                                                                                            Score 421.5; DB 1
Pred. No. 1.5e-19;
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/FTId=VSP_001149.
fW; 75FEA78FA8E48293 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (chondroitin sulfate)
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                                                                                                                                                                                                                                                                                                                                                                  Indels 105;
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(Potential).
(Potential).
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RESULT 14
Q4SD22 TETNG PRELIMINARY;
AC Q4SD22;
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A Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
A Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
A Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
A Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
A Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
A Anthonard V., Jubin C., Castelli V., Katlinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolic P., Poulain J., De Berardinis V.,
Biemont C., Skalli Z., Cattolic P., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
A Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
A Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
A Rellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
A Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
A Lindbad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
A Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
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Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
Mincker P., Lander E.S., Weissenbach J., R
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Best Local S
Matches 128
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13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Whole genome shotgun seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collagen;
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NON_TER
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodont.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00060; FN3; 11.
SMART; SM00327; VAB; 3.
PROSITE; PS50853; VAB; 3.
PROSITE; PS50234; VWFA; 3.
Collagen; Extracellular matrix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Fragment).
ORFNames=GSTENG00020231001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary data.
EMBL; CAAE01014645; CAG01460.1; -;
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PRINTS; PR00453; VWFADOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00041; fn3; 11. Pfam; PF00092; VWA; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003961; FN_III.
InterPro; IPR003962; FNIII_s
InterPro; IPR002035; VWF_A.
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                                                                                                                                                                                                                                                           436
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                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                 SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVMVTDGGSSDPV
                                                                                                                                                                                                                                                           RGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQH
QEPAANLRNSDVEIFAVGVKDAVRSELEAIANAPAETHVYTVEDFDAFQRISTELTQSIC
                                                                 GPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKH------
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 411.5; DH 2.
                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7EB78DA80D1E6B40 CRC64;
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RESULT 15
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15-JUL-1998 (Rel. 36, C
28-FEB-2003 (Rel. 41, I
10-MAY-2005 (Rel. 47, I
                                                                                                                                           "Structural variation of type XII collagen at its carboxyl-terminal NC1 domain generated by tissue-specific alternative splicing.";
J. Biol. Chem. 274:22053-22059 (1999)
-:- FUNCTION: Type XII collagen interacts with type I collagen-containing fibrils, the COL1 domain could be associated with the surface of the fibrils, and the COL2 and NC3 domains may be localized in the perifibrilar matrix (By similarity).
-:- SUBUNNIT: Triner of identical chains each containing 190 kDa of
                                                                                                                                                                                                                                                                                                                                             AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                   -
                                                                                                                                                                                                                                                                            STRAINE-C57BL/6J; TISSUE-Skin fibroblast;
MEDLINE-99348349; PubMed=10419532; DOI=10.1074/jbc.274.31.22053;
Kania A.M., Reichenberger E., Baur S.T., Karimbux N.Y., Taylor R
Olsen B.R., Nishimura I.;
                                                                                                                                                                                                                                                                                                                                                           PARTIAL NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                           development."
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96170761; PubMed=8601036;
Boehme K., Li Y., Oh P.S., Olsen B.R.;
"Primary structure of the long and short splice variants of mouse collagen XII and their tissue-specific expression during embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J, and Swiss Webster; TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collagen alpha 1(XII)
Name=Coll2a1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE, AND ALTERNATIVE SPLICING (ISOFORMS
                                                                                Event=Alternative splicing; Named isoforms=4; Comment=The final tissue form of collagen X
                                                                                                                  nontriple-helical sequences (By similarity). ALTERNATIVE PRODUCTS:
                  Name=XIIA-2; Synonyms=ER#K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  849
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                                 IsoId=Q60847-1; Sequence=Displayed;
                                                                   homotrimers or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGPLRGGEAQRVEVPAGRNCTTLQGLAPGTAYLVTVTAAFRSGRESALSAKACTPD--GP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VALVPESNVRLLRPQILRVRTRPEEAGPERIVISHARPRSLRVSWAPALGSAAALGYHVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POSFRVSWRAAPGAVARYRL----TYQPAGAGEAQLEAFTAGPELTMVLQDLQPRTTYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSGFRLAWPPLLTADSGYYVLELVPSAQPGAARRQQL----PGNATDWIWAGLDPDTDYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMSVPGDVLTALLPHLTPLTRYEVSVSAQYAKGTSLPVTGYGTTAEERGSVQNLKVTEES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VOELRGSILDAMRP
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                                                                                                                                                                                                                                                                                                                                                                                            204:432-445(1995).
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                                                                   any combination
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Last annotation update)
chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
 Sequence=VSP_001151,
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VSP_001152,
                                                                 various
                                                                                   XII may contain
                                                                   isoforms;
                                                                                                                                                                                                                                                                                                                                                            (ISOFORMS XIIA-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XIIA-1
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                                                                                                                                                                                                                                                                                           R.W.,
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     Glycoprotein;
SIGNAL
CHAIN 2
 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002035; VWF A. Pfam; PF01391; Collagen; 4. Pfam; PF00041; fn3; 18. Pfam; PF00092; VWA; 4.
                                                                                                                                                                                                                                                                                                          PROSITE; PS50853; FN3; 18.
PROSITE; PS50234; VWFA; 4.
Alternative splicing; Cell adhesion; Collagen;
                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00453; VWFADOMAIN
SMART; SM00060; FN3; 18.
SMART; SM00210; TSPN; 1.
SMART; SM00327; VWA; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U25652; AAA99719.1; ALT_SEQ; EMBL; U57095; AAB07047.1; -; mRNA. HSSP; P18614; 1MHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This Swiss-Prot entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      + + +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003129; Laminin_G_TSP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005615; C:extracellular space; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ensembl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chondroitin-sulfate type (By similarity).

SIMILARITY: Belongs to the fibril-associated collage interrupted helices (FACIT) family.

SIMILARITY: Contains 18 fibronectin type-III domains SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain. SIMILARITY: Contains 4 VWFA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          skin, cornea, sclera, blood vessels, and periosteum. DEVELOPMENTAL STAGE: The long NC3 XIIA isoforms are predominant at early stages (ED7 and 11); at later stages of development (ED15 and 17) the short NC3 XIIB forms become the major forms. As the short NC3 forms become the major product, the long splice variant continues to be expressed in several tissues, even after birth. The long NC1 isoforms, XIIA-1 and XIIB-1, peak in 15-day old embryos and decrease in 17-day old ones. The expression of the short NC1 form XIIB-2 remains constant throughout late stages of embryonic development (ED15 and ED17).

PTM: The triple-helical tail is stabilized by disulfide bonds at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              each end (By similarity). Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: Highest expression skin, cornea, sclera, blood vessels, ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: 0-glycosylation of isoform XIIA-2; glycosaminoglycan of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=XIIB-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:88448; Coll2al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q60847-4; Sequence=VSP_001150,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q60847-3; Sequence=VSP_001150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   long as its content is in no way modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENSMUSG00000032332; Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR003961; FN_III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR008160;
                                                1090
1203
1388
1478
                                                                                                                                                                                                                                                                                           Hydroxylation;
   3119
112
316
422
620
620
723
814
997
1087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collagen.
               Fibronectin
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Fibronectin
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                                                                                   VWFA
                                                                                                                                                 Fibronectin
                                                                                                                                                               Fibronectin
                                                                                                                                                                                             VWFA 2.
                                                                                                                                                                                                              Fibronectin
                                                                                                                                                                                                                                              Collagen alpha 1(XII)
Fibronectin type-III
                                                                                                                                                                                                                                                                                         Repeat;
                                                                                                                                                                            Fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA.
                                                                                                                                                                                                                                                                                           Signal; Structural protein.
     type-III
type-III
type-III
type-III
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type-III
                                                                                               type-III
type-III
type-III
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type-III
                                                                                                                                                                                                              type-III
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                                                                                                                                                                                                                                                                                                             Extracellular matrix;
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11.
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DOMALN 1849 1937	유 성	유	유성	유	M B Q	SOFT	333	3333	444	17.	333	337	3 T ;	F F .	Į Į	ŦŦ	ŦŢ	1 T	33	H .	3	Į,	F.H.	H.	ŢŢ,	P P	F F F		377]] ;	33	I. i.
Hay 1937 Fibromectin type-III 14. 1399 2019 Fibromectin type-III 16. 2211 2218 Fibromectin type-III 16. 2212 2229 Fibromectin type-III 18. 2229 2291 Fibromectin type-III 18. 2229 2292 Fibromectin type-III 18. 2393 Fibromectin type-III 18. 2393 Fibromectin type-III 18. 2393 Fibromectin type-III 18. 2394 Fibromectin type-	190	130 540		23 420	ery Match st Local tches 12)UENC	VARSPLIC	VARSPLIC	CARBOHYD VARSPLIC	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD	CARBOHYD	MOD_RES	MOD_RES	MOD_RES	MOD_RES	MOD_RES	MOD_RES	MOD_RES	MOD_RES	ים, נט		MOTIF	REGION	REGION	REGION	DOMAIN	DOMAIN	DOMAIN	DOMAIN
Fibronectin type-III 14. Fibronectin type-III 15. Fibronectin type-III 16. Fibronectin type-III 16. Fibronectin type-III 17. Fibronectin type-III 17. Fibronectin type-III 18. WFA 4. TSP N-terminal. Nonhelical region (NC1). Triple-helical region (CC2) with 1 imperfection. Cell actachment site (Potential). Cell attachment site (Potential). Hydroxyproline (By similarity). Hydrox	LHFV-DVI	GARPGVPI : GSRSNVPI	ALRASLVI :: RVQISLV	RGPPAS : : KTQPKI	imilari ; Cons	119	90	90	•	I CO N	ı	985	893	802	3030 704	3024 3027	3015	3001	2972 2984	2969	2960	2948 2951	869 2945	2896	3784	3046	യയ	75	500	22 5	53	93
Fibronectin type-III 14. Fibronectin type-III 15. Fibronectin type-III 16. Fibronectin type-III 17. Fibronectin type-III 18. WFA 4. TSP N-terminal. Nonhelical region (NC2). Triple-helical region (COL2) with 1 imperfection. Nonhelical region (NC2). Triple-helical region (COL1) with 2 imperfections. Nonhelical region (NC2). Triple-helical region (NC2). Nonhelical region (NC2). Triple-helical region (NC2). Triple-lelical region (NC2). Triple-helical region (NC2). Triple-helica	DDLHIIVQE DAFQRISFV	KVLVWVTDG :::: KVMILITDG	HVGSRPYTE : QYSRDPHTE	AP OPMKVQVEC	18.9 Y 28.7 rvative	ω.	3119	90	19	53	76	985	893	802	3030 · 704	3024	3015	3001	2972 2984	2969	2960	2948 2951	.2945	2898	3786 868		94	m ~	1 -1 11	4 (1 7	\sim	0 10
	ILDAMRPQQLHATEITSSGFRLAWPPL 2	SDPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKH 1 	FPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEAS 1 	0 4	\$; Score 407; DB 1; Length 3119;\$; Pred. No. 1.5e-18;64; Mismatches 177; Indels 60; Gaps 10	/FTId=VSP_001152. /FTId=VSP_001152. 4 MW; 9B1F999C86AB3251 CRC6	3P 001151. (In isoform XIIA-2 and isofo	3P 001150. 3SG (in isoform XIIA-2 and isof	(in isoform XIIB-1 and isof	inked (GlcNAc) (Potential	inked (GloNAc) (Potent	idl). (Chondroitin sulfat	(Xyl) (chondroitin sulfat	(1) (chondroitin sulfate	Hydroxyproline (By similarity). N-linked (GlcNAc) (Potential	Hydroxyproline (By sim Hydroxyproline (By sim	(By sim	(By sim	(By sim	line (By sim	line (By sim	line (By sim: line (By sim:	(By sim	attachment site (Potential)	attachment site (Potential)	ion (NC1)	ion (NC2).	region (COL2) with		type-III	type-III	type-III type-III

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Search completed: February 13, 2006, 07:47:47 Job time : 331.926 secs

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Aae32502 Human Wil
Abp69674 Human pol
Adn71106 Human pro
Aae32501 Mouse Wil
Aaw86326 Kidney in
Aab42581 Human ORF
Aab88340 Human gen
Ady63045 Human gen
Ady65347 Human alb
Adl78614 Albumin f
Aab87424 Human gen
Abg65347 Human alb
Adl78614 Albumin f
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Aab87424 Human ext
Aae32503 Human von
Aae03654 Human von
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264	268.5	268.5	268.5	270	272.5	284.5	326	326	360	382.5	382.5	382.5	382.5	382.5	382.5	384	392.5	392.5	92	392.5	
12.3	12.5	12.5	12.5	12.5	12.7	13.2	15.1	15.1	16.7	17.8	17.8	17.8	17.8	17.8	17.8	17.8	18.2	18.2	18.2	18.2	
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ALIGNMENTS

RESULT 1
AAE32502
ID AAE3

AAE32502 standard; protein; 418

A

AAE32502;

24-MAR-2003

(first entry)

Human Willebrand Factor A domain related-protein (WARP).

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ZSXEFFF
PRO XXX PRAXX PRAX
WPI; 2003-111873/10
N-PSDB; AAD50399.
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                                                                                                                                                                                                                                                                                                                                                                                                                       07-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disulfide-bond
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                                                                                                       Bateman JF, Fitzgerald DJ;
                                                                                                                                                                                                                                                           02-MAY-2001; 2001AU-00004701.
                                                                                                                                                                                                                                                                                                                                           02-MAY-2002; 2002WO-AU000542
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                                                                                                                                                                                   (MURD-) MURDOCH CHILDRENS RES INST.
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369. .393
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359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361
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RESULT 2
ABB69674
ID ABB7
XX ABP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Willebrand Factor A-Related Protein polypeptide useful for the manufacture of a medicament in the treatment of a disease condition of the extracellular matrix, in particular arthritis.
                                                                                                                                                                                         multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
                                                                                                                                                                                                                                      Human; genome mapping; gene therapy; food supplement; virus; cell-proliferative disorder; neurodegenerative disease; bacte Parkinson's disease; Alzhelmer's disease; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 418
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                                                                                      arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
haemostatic; vulnerary; fungicide; antibacterial; virucide; protozo
                                                                                                                                                                                                                                                                                                                                                                                                       Human
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                                                 antiarthritic.
                                                                                  haemostatic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             418;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEQLFAEASGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MLPWTALGLALSLRLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTLQGLAPGTAYLVTVTAAFRSGRESALSAKACTPDGPRPRPRPVPRAPTPGTASREP 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRPEEAGPERIVISHARPRSLRVSWAPALGSAAALGYHVOFGPLRGGEAQRVEVPAGRNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AASAPAEKHLHFVDVDDLHIIVQELRGSILDAMRPQQLHATEITSSGFRLAWPPLLTADS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                  fungicide;
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Pred. No. 2.6e-179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                   rus; fungus; bacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           418;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated polynucleotide (I) comprising a concleotide sequence selected from any of 948 sequences (ABZ11119-CC ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for cidentifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight maturers, as a food supplement, for generating antibodies, in medical cimaging, screening and diagnostic assays and for treating cell-crossing treative diseases, autoimmune diseases (Multiple sclerosis, cor alzheimer's disease), autoimmune diseases (multiple sclerosis, cor alzheimer's disease), autoimmune diseases (multiple sclerosis, liver cor lung fibrosis, infections (bacterial, viral, fungal, parasitic), cor lung fibrosis, infections (bacterial, viral, fungal, parasitic), cor the printed specification, but was obtained in electronic format cor directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; SEQ ID NO 1721; 1012pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-759812/82.
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301
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418; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                MLPWTALGLALSLRLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             445
                                                                                                                                                                                                                                                                                                            VAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYA
                                                                                          GYYVLELVPSAQPGAARRQQLPGNATDWIWAGLDPDTDYDVALVPESNVRLLRPQILRVR
                                                                                                                                                                                                                 KEQLFAEASGARPGVPKVLVMVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSA
                                                                                                                                                                                                                                      KEQLFAEASGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSA
                                                                                                                                                                                                                                                                                         VAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYA
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                 MLPWTALGLALSLRLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQL
TRPGEAGPGASGPESGAGPAPTQLAALPAPEEAGPERIVISHARPRSLRVSWAPALGSAA
                                                                     GYYVLELVPSAQPGAARRQQLPGNATDWIWAGLDPDTDYDVALVPESNVRLLRPQILRVR
                                                                                                                                             AASAPAEKHLHFVDVDDLHIIVQEI
                                                                                                                                                                               AASAPAEKHLHFVDVDDLHIIVQELRGSILDAMRPQQLHATEITSSGFRLAWPPLLTADS
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.9%;
93.9%;
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Pred. No. 3.2e-177;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence Listing;
                                                                                                                                             RGSILDAMRPQQLHATEITSSGFRLAWPPLLTADS
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RT;
                              PEEAGPERIVISHARPRSLRVSWAPALGSAA
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Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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, Ghosh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
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03-JUN-2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPDGPRPRPRPVPRAPTPGTASREP 445
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                    2002US-0385120P

2002US-0386741P

2002US-0386047P

2002US-038645P

2002US-038645P

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2002US-0386971P

2002US-0386971P

2002US-0386971P

2002US-0386971P

2002US-0386971P

2002US-0387400P

2002US-0387765P

2002US-038765P

2002US-038785P

2002US-038785P

2002US-038785P

2002US-038785P

2002US-038785P

2002US-0389784P

2002US-0389120P

2002US-0389146P

2002US-038974P

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21-JUN-2002; 2002US-0390763P.
17-JUL-2002; 2002US-04052BP.
06-AUG-2002; 2002US-0402156P.
09-AUG-2002; 2002US-0402359P.
19-AUG-2002; 2002US-0402359P.
12-AUG-2002; 2002US-0402332P.
12-AUG-2002; 2002US-0402332P.
13-AUG-2002; 2002US-0403331P.
13-AUG-2002; 2002US-0403331P.
13-AUG-2002; 2002US-0403563P.
13-AUG-2002; 2002US-04055532P.
13-AUG-2002; 2002US-040555P.
26-AUG-2002; 2002US-0406517P.
26-AUG-2002; 2002US-0406517P.
26-AUG-2002; 2002US-0406517P.
26-AUG-2002; 2002US-0406517P.
26-AUG-2002; 2002US-0406517P.
27-AUG-2002; 2002US-0406517P.
28-EP-2002; 2002US-0406517P.
29-SEP-2002; 2002US-0406517P.
20-SEP-2002; 2002US-040651P.
20-SEP-2002; 2002US-0416319P.
20-SEP-2002; 2002US-0414839P.
30-SEP-2002; 2002US-0414840P.
30-SEP-2002; 2002US-0414840P.
30-SEP-2002; 2002US-0414840P.
30-SEP-2002; 2002US-0414894P.
09-OCT-2002; 2002US-041786P.
23-OCT-2002; 2002US-041786P.
23-OCT-2002; 2002US-0423798P.
05-NOV-2002; 2002US-0423798P.
15-NOV-2002; 2002US-0423798P.
16-NOV-2002; 2002US-0423798P.
16-NOV-2002; 2002US-042353P.
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Gusev . Maclachlan T, Padigaru M, Rieger DK, Smithson G, Alsobrook JP, Catterton E, (Ettenberg S, (Gusev VY, Her Zhong Herrmann JL, T, Malyanka Patturajan M, Pena CEA, Peyman JA, Rothenberg ME, Sciore P, Shenoy SG, Spytek KA, Stone DJ, Vernet CAM, V , Alvarez E, Anderson DW, Boldog FL, Casman Chapoval A, Crabtree-Bokor JR, Edinger SR, Gangolli EA, Gerlach VL, Gorman L, Gunther errmann JL, Ji W, Kekuda R, Li L, Liu X, Wa , Malyankar UM, Mezick AJ, Millet I, Mishra Voss EZ, Raha D, Ras Shimkets RA; , Casman SJ;
nger SR, Ellerman
Gunther E, Guo Mishra VS; x, Macdougall Rastelli L; 3 × ű,

WPI; 2004-081935/08. N-PSDB; ADH71105.

New NOVX polypeptides and nucleic acid molecules useful for preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

Example 1; SEQ ID NO 2; 1880pp; English.

The invention relates to a novel isolated polypeptide (NOVX). A CC polypeptide of the invention has cytostatic, immunomodulator, neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and cc antilipaemic activity, and may have a use in gene therapy, and as a cc vaccine. The polypeptides are encoded by NOVX polymucleotides comprising a pecification. The polypeptide is useful in the manufacture of a medicament for treating a syndrome associated with a human disease. The polypeptide and antibody are useful in diagnosing, and treating or preventing NOVX-associated disorders, e.g. cancer, cachexia, Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present sequence crepresents a NOVX polypeptide of the invention.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse Willebrand Factor A domain related-protein (WARP).
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                     /note= "0-glycosylation site"
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                                                                                                                                                                                                                                                                                                                        /label=_Signal_peptide
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Matches 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (WARP) which is a member of von Willebrand Factor A domain related-protein superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The present sequence is mouse WARP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Willebrand Factor A-Related Protein polypeptide useful for the manufacture of a medicament in the treatment of a disease condition of the extracellular matrix, in particular arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 415 AA;
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                                                                                                    TRPEEAGPERIVISHARPRSLRVSWAPALGSAAALGYHVQFGPLRGGEAQRVEVPAGRNC
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                                                                                                                                                                                                                                                                   The present sequence represents a kidney injury associated molecule (KIM) CC protein. KIM proteins can be administered therapeutically by expressing CC KIM encoding polynucleotides, to promote growth and/or survival of CC damaged tissue (e.g. renal tissue), since the KIM proteins are uprespulsated in injured or regenerating (especially renal) tissues. KIM CC fusion proteins, conjugates, antibodies and vectors can also be used CC therapeutically, e.g. these or the KIM proteins may be included with an acceptable carrier in pharmaceutical compositions, useful for therapy/CC prophylaxis of conditions associated with disfunction/disregulation of CC KIM genes or proteins, especially renal diseases or impairments of renal function in humans (e.g. acute renal diseases or impairments of renal CC polynucleotides can be used to produce antisense sequences which, when CC internalised into cells, can disrupt expression of a cellular KIM gene, also useful in therapy (e.g. to block the growth of tumours dependent on CC MIM for growth) or compositions. The proteins and polynucleotides are CC useful diagnostically e.g. to detect and quantify renal injury or impaired function), or abnormal responses to tissue injury (indicative of increased risk, or presence of, renal injury or impaired CC increased risk, or presence of, an autoimmume response or abnormal tissue of cused to locate KIM-producing/expressing KIM such as tumours arising CC from/affecting renal tissue), by contacting cells with an imageable KIM-cCC binding reagent and imaging reagent accumulation
                                                                                                                                                                       Query Match
Best Local S
Matches 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kidney injury-associated molecule, KIM, injured or regenerating tissues, useful
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23-MAY-1997;
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                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                             421
                                                               VAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYA
                                                                                                                      MLPWTALGLALSLRLALARSGAERGPPASAPRGDLMFILDSSASVSHYEFSRVREFVGQL
 KEQLFAEASGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSA 180
                                    VATMPFGPGALRASLVHVGSRPHTEFTFDQYSSGQAIQDAVRVAPQRMGDTNTGLALAYA
                                                                                                      MLFWTVLSMALSLRLALAQSGIERGPTASAPQGDLLFLLDSSASVSHYEFSRVREFVGQL
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                                                                                                                                                                       31;
                                                                                                                                                                                       Score 1643.5; DB 2
Pred. No. 1.1e-134;
                                                                                                                                                                       Mismatches
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RESULT 6
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02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antiferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                      Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                    WPI; 2000-602362/57.
N-PSDB; AAC76790.
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                                         Claim 11; Page 3880-3881; 5507pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombosis; contraceptive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTLQGLAPGTAYLVTVTAAFRSGRESALSAKACTPDGPRPRPRPVPRAPTPGTASREP 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLQEEAGPERIVISHTRPRSLRVSWAPALGPDSTLGYLVQLGPLQGGSLEHVEVPAGQNS
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                                                                                                                                                                                                                                              2000US-00540763
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99US-0127636P.
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to which represent the human ORFX open reading frames 1 to 3161.

The ORFX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                 08-JUL-1999; 99JP-00194179.
11-JAN-2000; 2000JP-00118775.
02-MAY-2000; 2000JP-00183766.
                                                                                                                       07-JUL-2000; 2000EP-00114090
                                                                                                                                                                                         EP1067182-A2
                                                                                                                                                                                                                                                           Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes.
                                                                                                                                                                                                                                                                                                               Human membrane
                                                                                                                                                                                                                                                                                                                                                                                                                     AAB88340 standard;
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                                                                                                                                                         10-JAN-2001
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                   (HELI-) HELIX RES INST
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                                                                                                                                                                                                                                                                                                             or secretory protein clone PSEC0053
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93.2%;
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Pred. No. 2.7e-110;
0; Mismatches 16;
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Gene therapy

Human clone PSEC0053 protein,

SEQ

ij

02-JUN-2005

(first entry)

ADY63045

standard; protein;

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RESULT 8
ADY63045
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AC ADY6
XT
O2-J
XX
DE Huma
XX
KW Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cc which encode human secretory or membrane proteins represented by AAB8317 c AAB88419. Included in the invention are primers AAF93917 - AAF94295 and CC AAF62232 - AAF62235 which are used to isolate the CDNA sequences of the CC invention. The invention also includes methods for the production of CC antibodies directed against the proteins, and cDNA sequences, which can CC be used in vaccines. The polynucleotide sequences can be used in gene CC used in the prevention, treatment and diagnosis of diseases associated CC with inappropriate secretory protein/membrane protein expression. The CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. CC They may also be used as antigens in the proteins/membrane polypeptides and their role in metabolism. The CC polypeptides may be used as antigens in the production of secretory cotains/membrane polypeptides and their role in metabolism. The CC polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and CC antagonists) of expression and activity. The antibodies and antagonists of detecting the presence of the polypeptides in samples (e.g. by enzyme CC linked immunosorbant assay (ELISA). Examples of diseases which may be CC treated include rheumatoid arthritis and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Sim
Matches 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-093989/11.
DB; AAF93767.
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                                                                                                                                                                                                                                                     GYYVLGLVPSAQPGGCKTPAAARER
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96.6%;
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Pred. No. 6.7e
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Best Local Sim:
Matches 256;
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11-JAN-2000;
02-MAY-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane proteins, and their coding sequences. The present sequence is one such protein sequence. The coding sequences of the invention are useful for examination and diagnosis of abnormality of the human secretary proteins and in gene therapy methods. The coding sequences and proteins are useful as candidates for medicines or as target molecules for developing medicines. Antibodies against the proteins of the invention are useful for treating diseases that are associated with the proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained from sequence information
               22-MAY-2001
                                         AAB87344;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated polynucleotide encoding human secretary proteins or membrane proteins, useful for examination and diagnosis of abnormality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention relates to novel human secretory proteins or
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                                                                   standard;
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                                                                                                                                      GYYVLGLVPSÄQPGGCKTPAAARER 265
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2000JP-00183766.
2000EP-00114090.
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Pred. No. 6.7e-104;
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Human gene 3 encoded secreted protein HNTEO78, SEQ ID NO:85.

Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder, Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder, kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification.
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WO200118022-A1.
15-MAR-2001.
31-AUG-2000; 2000WO-US024008.
03-SEP-1999; 99US-0152315P.
03-SEP-1999; 99US-0152317P.
(HUMA-) HUMAN GENOME SCI INC.
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Ni J, Baker KP, Birse CE, Fiscella M, Komatsoulis GA, Rosen CA; Soppet DR, Young PE, Ebner R, Duan DR, Olsen HS, Lafleur DW; Moore PA, Shi Y, Wei Y, Florence KA; WPI; 2001-203081/20.

N-PSDB; AAF91860.

Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.

Claim 11; Page 532-533; 607pp; English.

AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB8744-AAB87443 represent the proteins they encode. AAB87414-AAB8745 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the protein for the new genes. Specific uses are described for each of the 2 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, parkinsonns's disease), organitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell counture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in indiagnostic immunoassays e.g., radioimmunoassays or enzyme linked immunoassays e.g., radioimmunoassays or enzyme linked immunoassays or enzyme linked immunoassays or enzyme linked immunoassays compared in the invention

Best Local Similarity

50.3%;

Score Pred.

1084; No. 3.

DB 4; .4e-86;

Length

Query Match

Sequence

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ARBSULT 10
ABG65347
ID 68465
AC ABG65
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                      The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HAA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitie, immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Albeimer's, payrings).
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25-APR-2000; 2000US-0199384P
21-DEC-2000; 2000US-0256931P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human albumin fusion protein #2022.
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        haematopoietic disorders, neur
Parkinson's, Creutzfeldt-Jacob
                                                                                                                                                                                                                                                                                                                                 Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-APR-2001; 2001WO-US011988
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Best Local (
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                                                                             New albumin fusion proteins, useful for diagnosing, or ameliorating diseases or disorders e.g. cancer, asthma, inflammatory bowel disease or Alzheimer's di
                                                                                                                                                                                                                                                                                                                          Unidentified
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21-DEC-2000;
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                                                                                                                                                                                                                                  12-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                  reproductive system disorder; therapeutic protein.
                                                                                                                                                                                                                                                        L2-APR-2001;
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2000US-0199384P.
2000US-0256931P.
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                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic;
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Pred. No. 3.
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                                                                                           arthritis,
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The invention relates to a novel albumin fusion protein. The inv further relates to: a composition comprising the albumin fusion and a pharmaceutical carrier; a kit comprising the composition or albumin fusion protein formula; a method of treating a disease of albumin fusion protein formula; a method of treating a disease of albumin fusion protein formula; a method of treating a disease of albumin fusion protein formula; a method of treating a disease of albumin fusion protein formula; a method of treating a disease of albumin fusion protein formula; a method of treating a disease of albumin fusion protein formula; a method of treating a disease of albumin fusion protein.

invention on protein of the

Disclosure;

SEQ

IJ

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2096;

279pp; English

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CC disorder in a patient comprising the step of administering the albumin CC that is modulated by Therapeutic protein: X, or its fragment or variant; CC a method of extending the shelf life of Therapeutic protein: X or its fragment or variant; a nucleic acid molecule comprising a polynucleotide CC sequence encoding the albumin fusion protein; a vector comprising the nucleic acid molecule of the albumin fusion protein; and a host cell CC comprising the nucleic acid molecule of the albumin fusion protein. The CC albumin fusion protein and its compositions have the following CC activities: cytostatic, antianaemic, antiarthritic, antiasthmatic, anti-ccell CC cardiant, nootropic, antilpaemic, nephrotropic, untiasthmatic, antiarrhythmic, CC cardiant, nootropic, antilpaemic, nephrotropic, uropathic, cardiant, nootropic, antipaemic, nephrotropic, uropathic, anabolic, hypertensive, and vulnerary. The albumin fusion protein nucleic acid may be used in gene therapy to treat disorders. The albumin fusion protein is cuseful for disgnosing, treating, preventing or ameliorating diseases or cisorders comprising indication: Y. The diseases or disorders include: cancer (e.g. leukaemia, colon, bone, breast, liver or lung cancer), compositic diseases (e.g. anaemia, Hodgkin's disease, acute lymphocytic anaemia, multiple myeloma, arthritis, asthma, AIDS, autoimmune disease, inflammatory bowel disease, psoriasis or Lyme classase; or cachexia, variaccele, penile carcinoma, ovarian adenocarcinoma or Sertoli-leydig tumours), musculoskeletal diseases (e.g. rhabdomyomas heart disease, colon, bone, branch, gout, muscular dystrophy or cachexia), cardiac arrest, heat valve disease, hypernatraemia or hyporatraemia or syndrome, pateus vyndrome, beat disease, c.g. rhabdomyomas, heart disease, c.g. conditions or syndrome, heart disease (e.g. rhabdomyomas, heart disease, c.g. rhabdomyomas, heart disease (e.g. rha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Down's Byndrome, Patau Syndrome, Turner's Syndrome, Apert Syndrome or Tay -Sachs disease), excretory diseases (e.g. urinary incontinence, urinary tract infections or renal disorders), neural or sensory disease (e.g. Alzheimer's disease, Parkinson's disease, cerebral malaria, meningitis, cerebellar ataxia, attention deficit disorder, autism or obsessive compulsive disorder), respiratory disease (e.g. emphysema, lung cancer or occupational lung disease), endocrine diseases (e.g. diabetes, Addison's disease or glomerulonephritis), digestive diseases (e.g. portal hypertension, irritable bowel disease, gastric atrophy or pancreatitis) or connective tissue or epithelial diseases (e.g. Crohn's disease, scleroderma, wound healing or epidermolysis bullosa). This sequence represents a therapeutic protein x relating to the albumin fusion protein of the invention. The sequence listing data for this specification was dowloaded from the USPTO website.
51
                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                  MLPWTALGLALSLRLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQL
                                                                                                       MLPWTAXGLALSLRLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQL
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Pred. No. 3.4e-86;
0; Mismatches 1;
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В Ś 밁 Ś 밁 S Query Match Best Local 181 121 121 61 AASAPAEKHLHFVDVDDLHIIVQELRGSILDAMRP 215 KEQLFAEASGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSA VAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYA VAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYA KEQLFAEASGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSA 180 180 120

RESULT 12 AAB87418 ፠ጽ፟፟፟፠ AAB87418 standard; protein;

> Human gene 3 encoded secreted protein fragment, (first

SEQ ID NO:159

foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; chemotaxis; food additive; binding partner identification. secreted protein; proliferative disorder; cancer; tumour;

WO200118022-A1

31-AUG-2000; 2000WO-US024008

99US-0152315P. 99US-0152317P.

(HUMA-) HUMAN GENOME SCI INC

Ni J, Baker KP, Birse CE, Fiscella M, Soppet DR, Young PE, Ebner R, Duan DR, Moore PA, Shi Y, Wei Y, Florence KA; Komatsoulis Olsen HS, GA, Ros Lafleur Rosen eur DW; CA;

WPI; 2001-203081/20

preventing, treating or ameliorating Parkinson's diseases and cancers. Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's

Disclosure; Page 18; 607pp; English.

CC and their corresponding secreted proteins are useful for preventing, cc treating or ameliorating medical conditions, e.g., by protein or gene conterapy. Pathological conditions can be diagnosed by determining the gene camount of the new protein in a sample or by determining the presence of camount of the new genes. Specific uses are described for each of the cs genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of cambormalities, haematopoietic disorders, diseases of the immune system, cc allorgies, neurological disorders (e.g., rheumatoid arthritis), inflammation, cc allorgies, neurological disorders (e.g., Alzheimer's diseases, cancer, thunours, foetal and developmental cc disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cc ardiovascular disorders, anglogenic disorders, schizophrenia, asthma, skin cc disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cc gastrointestinal disorders, pregnancy-related disorders, endocrine cc disorders, and infections. The proteins can also be used to aid wound comborn, to maintain organs before transplantation, for supporting cell collure of primary tissues, to regenerate tissues, to identify their conjunte ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

CC Antibodies specific for a protein of the invention can be used in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked cc immunosorbent assay (ELISA). The present sequence represents a human cc secreted protein fragment referred to in the disclosure of the invention AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87342-AAB87413 represent the proteins they encode. AAB87414-AAB87454 represent human secreted protein fragments. The genes

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RESULT 13
AAB87424
ID AAB87
XX AAB87727
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XX AAB877
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                           AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87342-AAB87413 represent the proteins they encode. AAB87414-AAB87454 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the
                                                                                                                                                                                                                                                                                               Nucleic acid molecules encoding human secreted proteins, used preventing, treating or ameliorating a disorder, e.g. Alzheim Parkinson's diseases and cancers.
                                                                                                                                                                                                                                      Disclosure; Page 18; 607pp; English.
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03-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-AUG-2000; 2000WO-US024008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baker KP,
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Shi Y,
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99US-0152317P.
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Wei Y, F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
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ner R, Duan DR,
Florence KA;
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Olsen HS,
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CC Antibodies specific for a protein of the invention can be used in dispostic immunosassys e.g., radioimmunosassy or enzyme linked CC immunosassys (ELISA). The present sequence represents a human CC secreted protein fragment referred to in the disclosure of the invention
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Best Local Similarity
Matches 213; Conserv
                                                                                                                                                                                                                                         gene therapy; genetic disorder; adrenoleukodystrophy; leukaemia; Down's syndrome; cystic fibrosis; Gaucher's disease; myotonic dystrophy; sickle cell anaemia; thalassaemia; autoimmune disorder; adenocarcinoma; inflammatory disorder; acquired immune deficiency syndrome; AIDS; Addison's disease; allergy; anaemia; asthma; atherosclerosis; melanoma; Crohn's disease; diabetes mellitus; atopic dermatitis; lymphoma; cancer; glomerulonephritis; multiple sclerosis; Grave's dieease; osteoarthritis; osteoprosis; psoriasis; rheumatoid arthritis; ulcerative colitis; infection; cell proliferative disorder; actinic keratosis; myeloma; infection; cell proliferative disorder; actinic keratosis; myeloma;
                                                                                                                                                                                                                   arteriosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; extracellular matrix and cell adhesion molecule; XMAD
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                                                                                                             sapiens
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100.0%;
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                                                                                                                                                                                                                   anticonvulsant;
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Pred. No. 1.5e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell adhesion molecule-18 (XMAD-18).
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Location/Qualifiers
1. .171

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CC sequences and to create knock in humanised animals (pigs) or transgenic CC animals (mice or rats) to model human diseases. Oligonucleotide or longer fragments derived from the polynucleotide sequences may be used as CC elements on a microarray. Antibodies which specifically bind XMAD may be CC used for the diagnosis of disorders associated with the expression of CC XMAD, or in assays to monitor patients being treated with XMAD. Diseases CC diagnosed, prevented or treated include genetic disorders such as CC adrenoleukodystrophy, Down's syndrome, cystic fibrosis, Gaucher's CC diseases, myotonic dystrophy, sickle cell anaemia, thalassaemia, CC autoimmune/inflammatory disorders such as acquired immune deficiency CC syndrome (AIDS), Addison's disease, allergies, anaemia, asthma, CC atherosclerosis, Crohn's disease, diabetes mellitus, atopic dermatitis, CC osteoporosis, psoriasis, rheumatoid arthritis, ulcerative colitis, CC osteoporosis, psoriasis, rheumatoid arthritis, ulcerative colitis, and cancer including breast, bladder, bone marrow, brain and uterus CC cancer lenkagia adamocarcinoma lumphoma melaroma and melaroma and melaroma.
                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a human extracellular matrix and cell adhesion molecule (XMAD). The XMAD is used for screening a compound for effectiveness as an agonist or antagonist of XMAD. The identified agonist or antagonist are used for treating a disease or condition associated with decreased or increased expression of functional XMAD. The product of the conditional XMAD is a conditionally polynucleotides encoding XMAD are useful in somatic or germline gene therapy to correct a genetic deficiency, to express a conditionally lethal gene product and to express a protein which affords protection against intracellular parasites and also for diagnosis of disorders associated with expression of XMAD. They are also used for generating hybridisation probes useful in mapping the naturally occurring genomic companies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human extracellular matrix and cell adhesion molecules and polynucleotide sequences encoding them, useful for diagnosis, pretreatment of genetic, autoimmune and cell proliferative disorders
                                                                                                                                                                                                                                                                                          Sequence
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16-DEC-1999;
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                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 111; 135pp; English.
                                          MFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGE
MFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGE
                                                                                                                                                                                                                                                                                          185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DAM,
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99US-0172354P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Collagen glycoprotein precursor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lal P,
                                                                                                                                                                                                                                                                                                                                                               adenocarcinoma,
                                                                                                                                                                  42.6%;
100.0%;
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                                                                                                                                                                          Score 918;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Au-Young J;
                                                                                                                                                                                                                                                                                                                                                               lymphoma, melanoma and myeloma
                                                                                                                                   ; DB 4; I
. 8.9e-72;
ches 0;
                                                                                                                                                                                                            Length 185,
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Matches 180; Conser

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42.4%; Score 913; DB 6; 100.0%; Pred. No. 2.3e-71; tive 0; Mismatches 0;

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                                                            The invention relates to Willebrand Factor A domain related-protein (WARP) which is a member of von Willebrand Factor A (VA)-domain protein superfamily of extracellular matrix (ECM) proteins. WARP is used as a molecular marker, used for detecting a loss of ECM integrity in an animal subject, monitoring repair, regeneration or other disease processes in an animal subject and detecting a disease condition or a propensity for the development of a disease condition in an animal subject. The invention is useful for the manufacture of a medicament in the treatment of a disease condition of the ECM. The disease condition involves the cartilage, and is preferably arthritis. The invention is also used in gene therapy. The present sequence is human VA domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated Willebrand Factor A-Related Protein polypeptide useful for the manufacture of a medicament in the treatment of a disease condition of the extracellular matrix, in particular arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Encoded by GGG"
Misc-difference 179. .180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Willebrand Factor A domain related-protein; von Willebrand Factor A; VA; extracellular matrix; ECM; molecular marker; cartilage; arthritis; WARP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 72-73; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAY-2001; 2001AU-00004701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-2002; 2002WO-AU000542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
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DB; AAD50397.
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1. .2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Encoded by CTC"
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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein -
           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     DB DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA_Main:*

1    /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2    /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3    /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

4    /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5:    /cgn2_6/ptodata/1/pubpaa/US11B_PUBCOMB.pep:*

6:    /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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Gapop 10.0 , Gapext 0.5
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        GenCore version (c) 1993 - 2006
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                                                                                                       Sequence 4, Application US/10699035A Publication No. US20040214349A1 GENERAL INFORMATION:
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APPLICANT: Bateman, John
APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
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APPLICANT: Bateman, John
APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
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PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
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ORGANISM: Homo sapiens
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Pred. No. 2e-174;
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PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 4
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TYPE: PRT
ORGANISM: Mus musculus
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PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/10699035A Publication No. US20040214349A1 GENERAL INFORMATION:
    Matches
                     Query Match
Best Local
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APPLICANT: Fitzgerald, David
APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR FILING DATE: 2002-05-02
                                                                                                     ORGANISM: Mus
                                                                                                                             TYPE: PRT
                                                                                                                                              LENGTH: 415
324;
                         Similarity
    Conservative
                                                                                                       musculus
                     76.8%;
77.5%;
  32;
Score 1653.5;
Pred. No. 7.4e.
12; Mismatches
                         7.4e-132;
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Best Local Similarity
Matches 214; Conserv
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OTHER INFORMATION: Xaa equals any of the naturally occurring
-09-789-561-85
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CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
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TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: PZ043P1
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                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE LOCATION: (7)
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Homo sapiens
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o. US20020064818A1
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                                                             KEQLFAEASGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSA
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   AASAPAEKHLHFVDVDDLHIIVQELRGSILDAMRP 215
                                                                                                           VAPLPLGTGALRASLVHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYA
                                                                                                                                                                                MLPWTAXGLALSLRLALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQL
                                     KEQLFAEASGARPGVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSA
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Pred. No. 8.4e-84;
0; Mismatches 1
                                                                                                                                                                                                                                                                                    Length
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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino US-09-833-245-2096
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CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
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US-09-833-245-2096
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           CURRENT APPLICATION NUMBER: US/10/883,936
CURRENT FILING DATE: 2004-07-06
PRIOR APPLICATION NUMBER: US/09/789,561
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
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LENGTH: 215
TYPE: PRT
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Matches
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                                                                                                                                                                                                                                                                                                                                               Sequence 85, Application US/10883936
Publication No. US20050019866A1
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Best Local Similarity
                                                                                                                                                                                                                                     APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: PEO43P1
CURRENT APPLICATION NUMBER: US/10/883,936
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Pred. No. 8.4e-84;
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CURRENT APPLICATION NUMBER: US/09/789,561
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
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US-09-789-561-159
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; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-883-936-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: PZ043P1
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SOFTWARE: PatentIn V
SEQ ID NO 159
LENGTH: 242
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Best Local Similarity
                                                                     Matches
                                                                                                      Query Match
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                                                                                                                                          OTHER INFORMATION: Xaa equals any of the naturally occurring -09-789-561-159
                                                                                                                                                                                                                                                                          PEATURE:
NAME/KEY: SITE
NAME/KEY: (2)
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OTHER INFORMATION: Xaa e
NAME/KEY: SITE
LOCATION: (5)
OTHER INFORMATION: Xaa e
NAME/KEY: SITE
LOCATION: (34)
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                MLPWTALGLALSLRLALARSGAERGPPASAPRGDLMFILDSSASVSHYEFSRVREFVGQL
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                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Ver. 2.0
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                                                                     Conservative
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Pred. No. 8.4e-84;
                                                                                  Score 1084; DB 3;
Pred. No. 9.9e-84;
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PRIOR APPLICATION NUMBER: US/09/789,561
PRIOR FILING DATE: 2001-02-22
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
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US-10-883-936-159
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                                                                                                                                                                                                                                                                Matches 214;
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Best Local Similarity 99.5%;
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TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: PZ043P1
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CURRENT FILING DATE: 2004-07-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
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OTHER INFORMATION:
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AASAPAEKHLHFVDVDDLHIIVQELRGSILDAMRP 215
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Pred. No. 9.9e-84;
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CURRENT APPLICATION NUMBER: US/09/789,561
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR PFLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
SOPTWARE: PatentIN Ver. 2.0
SEQ ID NO 165
LENGTH: 226
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                                                                                                                                          PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 165
LENGTH: 226
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APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted proteins
Query Match
Best Local Similarity
Matches 213; Conserv
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/883,936
CURRENT FILING DATE: 2004-07-06
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US/09/789,561
PRIOR TLING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
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PRIOR FILING DATE: 1999-09-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: 52 Human secreted proteins
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                                                                                                                           TYPE: PRT
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50.0%; Score 1077; DB 5; 100.0%; Pred. No. 3.6e-83; ive 0; Mismatches 0;
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; OTHER INFORMATION: Incyte
US-10-149-819-18
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US-10-149-819-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 18
LENGTH: 185
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Best Local Similarity
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/172,852; 60/172,354
PRIOR FILING DATE: 1999-12-10; 1999-12-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL Program
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APPLICANT: BURFORD, Neil
TITLE OF INVENTION: EXTRACELLULAR MATRIX AND
FILE REFERENCE: PF-0760 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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181
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PATTERSON, Chandre
BAUGHN, Mariah R.
LU, Dyung Aina M.
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100.0%; Pr
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Pred. No. 9.1e-70;
0; Mismatches 0;
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RESULT

US-10-699-035A-2

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APPLICANT: FITZGETAID, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION UNMER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AJ002/00542
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FASTSEQ for Windows Version 4.0
SOFTWARE: FASTSEQ for Windows Version 4.0
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US-10-699-035A-31
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PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 31, Application US/10699035A Publication No. US20040214349A1 GENERAL INFORMATION:
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Best Local :
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APPLICANT: Fitzgerald, David
APPLICANT: Fitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
FURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR FILING DATE: 2002-05-02
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TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Homo sapiens
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SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 151
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100.0%; Pred. No. 2.3e-69;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                   35.8%; Score 772; DB 4; Length 181; 83.4%; Pred. No. 2.3e-57; 1tive 14; Mismatches 16; Indels
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GENERAL INFORMATION:
APPLICANT: Bateman, John
APPLICANT: Bateman, John
APPLICANT: Bitzgerald, David
TITLE OF INVENTION: A Molecular Marker
FILE REFERENCE: A36056 PCT USA A 071838.0142
CURRENT APPLICATION NUMBER: US/10/699,035A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/AU02/00542
PRIOR APPLICATION NUMBER: AU PR4701/01
PRIOR FILING DATE: 2002-05-02
PRIOR FILING DATE: 2001-05-02
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Best Local Similarity
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TYPE: PRT
ORGANISM: Mus
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                                                                                   SSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVPKVLVWVTDGGSSDPV 151
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GPPMQELKDLGVTIFIVSTGRGNLLELLAAASAPAEKHLHFVDVDDLPIIARELRGSITD
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                                                                                                                                                                                                                 Score 768; DB 4
Pred. No. 5e-57;
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Search completed: February 13, 2006, 13:12:40 Job time: 86.2776 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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Gapop 10.0 ,
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       Issued Patents AA:*
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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       GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration
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  US-09-513-999C-6277
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US-09-949-016-11341
US-09-949-016-11519
US-09-949-016-11520
US-09-949-016-11520
US-08-897-443-1
US-09-905-725A-34
US-09-906-700-34
US-09-906-700-34
US-09-906-700-34
US-09-906-618-34
US-09-906-618-34
US-09-906-618-34
US-09-906-618-34
US-09-906-618-34
US-09-906-618-34
US-09-906-618-34
US-09-906-722A-34
US-09-906-723A-34
US-09-906-723A-34
US-09-906-723A-34
US-09-906-723A-34
US-09-908-736A-34
US-09-908-736A-37
US-08-463-108-37
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Sequence 10340, A
Sequence 11311, A
Sequence 11520, A
Sequence 11520, A
Sequence 11520, A
Sequence 34, Appl
Sequence 37, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
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Result No.

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US-09-513-999C-6277
Sequence 6277, Application US/09513999C
Patent NO. 6783961
GENERAL INFORMATION:
                                                                                                                                               RESULT 2
US-09-919-497-57
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Sequence 57, Application US/09919497
PACENT NO. 6773883
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
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SOPTWARE: Patent.pm
SEQ ID NO 6277
LENGTH: 77
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 66
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                 168 VSTGRGNFLELSAAASA 184
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Pred. No. 1.
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                                                             ENDOMETRIAL CANCER
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; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 57
; LENGTH: 755
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-57
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10340
LENGTH: 584
TYPE: PRT
ORGANISM: Human
US-09-949-016-10340
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US-09-949-016-10340
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Best Local S
Matches 67
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,768
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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Best Local Similarity
468
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                                                                                                                                                                                                                               34 DIMFILDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS 93
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                                                                                                                                                                                                                                                                                                   Similarity
                                                                                         AAEVKQAVLAVEYMERGTMTGLALRHMVEHSFSEAQGARPRALNVPRVGLVFTDGRSQDD 467
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ISVWAARAKEEGIVMYAVGVGKAVEAELREIASEPAELHVSYAPDFGTMTHLLENLRGSI 527
                                        VGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGSI 209
                                                                                                                                      GEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARP----GVPKVLVWVTDGGSSDP 150
                                                                                                                                                                                    DLVILLVDGSKSVRPQNFELVKRFVNQIVDFLDVSPEGTRVGLVQFSSRVRTEFPLGRYGT
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                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                           12.0%; Score 259; DB 2; Length 584; 37.2%; Pred. No. 2.9e-14; tive 25; Mismatches 84; Indels
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Qy 5 TALGLALSIRL	Query Match 11.8%; Score 255; DB 2 Best Local Similarity 27.9%; Pred. No. 1.3e-1 Matches 68; Conservative 43; Mismatches	RESULT 5 US-09-949-016-11519 ; Sequence 11519, Application US/09949016 ; Patent No. 6812339 ; GENERAL INFORMATION: ; APPLICANT: VENTER, J. Craig et al. ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ; TILTE OF INVENTION: WITH HUMAN DISEASE, METHODS ; FILE REFERENCE: CL001307 ; CURRENT APPLICATION NUMBER: US/09/949,016 ; CURRENT FILING DATE: 2000-04-14 ; PRIOR APPLICATION NUMBER: 60/241,755 PRIOR FILING DATE: 2000-10-20 ; PRIOR APPLICATION NUMBER: 60/237,768 PRIOR APPLICATION NUMBER: 60/237,768 PRIOR APPLICATION NUMBER: 60/231,498 ; PRIOR APPLICATION NUMBER: 60/231,498 ; PRIOR FILING DATE: 2000-09-08 ; NUMBER OF SEQ ID NOS: 207012 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 11519 ; LENGTH: 963 ; TYPE: PRT ORGANISM: Human US-09-949-016-11519	Qy 151 VGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHLHFV-DVDDLHIIVQELRGS	Qy 94 GEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARPGVEKVLVWVTDGGSSDP	Qy 34 DLMFILDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFPFGQHSS	Query Match 12.0%; Score 259; DB 2 Best Local Similarity 37.2%; Pred. No. 2.9e-1: Matches 67; Conservative 25; Mismatches	RESULT 4 US-09-949-016-10341 Sequence 10341, Application US/09949016 Sequence 10341, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION: APPLICANT: VENTER, J. Craig et al. TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS FILE REFERENCE: CL001307 CURRENT APPLICATION NUMBER: US/09/949,016 CURRENT FILING DATE: 2000-04-14 PRIOR APPLICATION NUMBER: 60/237,768 PRIOR FILING DATE: 2000-10-20 PRIOR APPLICATION NUMBER: 60/237,768 PRIOR FILING DATE: 2000-10-03 PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10341 LENGTH: 584 TYPE: PRT ORGANISM: Human US-09-949-016-10341
30 ::: :	; DB 2; Length 963; 1.3e-13; ches 89; Indels 44; Gaps 4;	METHODS OF DETECTION AND USES THEREOF	AAASAPAEKHLHFV-DVDDLHIIVQELRGSI 209 :	ZLFAEASGARPGVPKVLVWVTDGGSSDP 150 :		; DB 2; Length 584; 2.9e-14; ches 84; Indels 4; Gaps 2;	METHODS OF DETECTION AND USES THEREOF

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US-08-897-443-1
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US-09-949-016-11520
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US-09-949-016-11520
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 11520
LENGTH: 963
Sequence 1, Application US/08897443 Patent No. 5981263
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Best Local 9
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTIO
FILE REFERENCE: CL001307
                                                                                                                                                       201 IVQE 204
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                                                                                                                                                                                                                                                                                                              88 FGQHSSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARP----GVPKVLVWVTD 144
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                                                                                                                                                                                                                                                                                                                                                     92 CENKRADLVFIIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFS
                                                                                                                                                                                                                                                                                                                                                                                          31 --- PRGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFP
                                                                                                                                                                                                                                                                                                                                                                                                                                     32 TALPLLLALKMEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPQTALLESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                              GRPQDSVAEVAAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTS
                                                                                                                                                                                                                                  GGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL----HFVDVDDLHI 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---PRGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASLVHVGSRPYTEFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TALPLLLALKMEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPQTALLESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 255; DB 2; Length 963; Pred. No. 1.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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RESULT 8
US-09-907-794A-34
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                                                        Sequence 34, Application US/09907794A Patent No. 6635468 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Hillman
APPLICANT: Lal, Pr
APPLICANT: Corley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, Davi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: UTRSNOT02
CLONE: 681719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/897,443
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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                                                                                                                                                                                                                                                                        159
                                                                                                                                                                                            219 VANÉSQIETLTSVEQK 234
                                                                                                                                                                                                                                191 --HFVDVDDLHIIVQE 204
                                                                                                                                                                                                                                                                                                          134 -GVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL-- 190
                                                                                                                                                                                                                                                                                                                                                  99 LQYGSTVKNEFSLKTFKRKSEVERAVKRMRHLSTGTMTGLAIQYALNIAFSEAEGARPLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 ALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASL
                                                                                                                                                                                                                                                                                                                                                                                    76 VHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARP-- 133
                                                                                                                                                                                                                                                                                                                                                                                                                              45 ALLESSCEN-----KRADLVFIIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       638 amino acids
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31.6%; Pred. No. 9.9e-14;
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218

Desnoyers, Eaton, Dan

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Query Match
Best Local Similarity
Whiches 62; Conserve
                                                                                               ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-907-794A-34
                                                                                                                                                      SEQ ID NO 34
LENGTH: 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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PPLICANT: Wood, William, I.
TILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1999-07-26
APPLICATION NUMBER: US 60/146,222
FILING DATE: 1999-07-28
APPLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
FILING DATE: 1999-10-05
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APPLICATION NUMBER: PCT/US99/28313
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                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US99/30999
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/30095
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US99/28565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US99/28214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US99/20944
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US99/28564
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Gao, Wei-Qiang
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Mather, Jennie P.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher
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                    Conservative
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art, Timothy A.
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f, Ellen
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                                    11.8%;
                    36;
                  Score 253.5; DB 2;
Pred. No. 1.6e-13;
6; Mismatches 85;
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                    Indels
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                                                                          PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR PELICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Secreted and Transmembrane Polypeptides TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
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                                                        OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: 1999-09-15
OR APPLICATION NUMBER: PCT/US99/21547
OR FILING DATE: 1999-09-15
OR APPLICATION NUMBER: PCT/US99/23089
OR FILING DATE: 1999-10-05
OR APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
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Botstein, David
Desnoyers, Luc
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Grimaldi, Christopher J.
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Stewart, Timothy A.
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Mather, Jennie P.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Filvaroff, Ellen
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RESULT 10
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LENGTH: 915
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local
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APPLICANT:
        APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
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Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Tvar J.
Mather, Jennie P.
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Botstein, David
                                                                                       Roy, Margaret Ann
Stewart, Timothy A.
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Gerritsen, Mary E.
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Filvaroff, Ellen
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Eaton, Dan L.
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10466-14
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ni, Nicholas F.
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Pred. No. 1.6e-13;
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US-09-906-700-34

Sequence 34, Application US/09906700 Patent No. 6723535 GENERAL INFORMATION:

APPLICANT: Genentech, Inc. APPLICANT: Ashkenazi, Avi APPLICANT: Botstein, David

APPLICANT:

Desnoyers,

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CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR,FILLING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
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SEQ ID NO 34
LENGTH: 915
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Best Local S
Matches 62
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
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PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
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PRIOR APPLICATION NUMBER: PCT
PRIOR FILING DATE: 1999-09-15
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PRIOR APPLICATION NUMBER: PCT/US99/20944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
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FILING DATE: 1999-12-02
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219 VANFSQIETLTSVFQK 234
                                               191 --HFVDVDDLHIIVQE 204
                                                                                            159 ENVPRVIMIVTDGRPQDSVAEVAAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFL
                                                                                                                                       134 -GVPKVLVWVTDGGSSDPVGPPMQELKDLGVTVFIVSTGRGNFLELSAAASAPAEKHL--
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                                                                                                                                                                                                                                                                          62;
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                                                                                                                              ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-906-700-34
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LENGTH: 915
                                                          Matches
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Best Local Similarity
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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PRIOR FILING DATE: 2000-02-2
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
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FILING DATE: 1999-07-26
APPLICATION NUMBER: US 60/146,222
FILING DATE: 1999-07-28
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APPLICATION NUMBER: PCT/US99/30911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US99/20944
                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US99/23089
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US99/30999
16 ALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASL
                                                        62; Conservative
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Mather, Jennie P.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher
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ira, Napoleone
--off, Ellen
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                                                      11.8%; Score 253.5; DB 2; 31.6%; Pred. No. 1.6e-13; tive 36; Mismatches 85;
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RESULT 12
US-09-903-603A-34
US-09-903-603A-34
C7676
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CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: CT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-09-08
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Patent No. 6767995
GENERAL INFORMATIO
APPLICANT: Genent
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FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
APPLICATION NUMBER: PCT/US99/28564
                                                                                                              FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
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APPLICATION NUMBER: PCT/US99/21090
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Williams, P. Mickey
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Gao, Wei-Qiang
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Mather, Jennie P.
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Grimaldi, Christopher J.
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Eaton, Dan L.
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Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan, James
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILLING DATE: 1999-12-16
PRIOR FPLICATION NUMBER: PCT/US99/30911
PRIOR FILLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILLING DATE: 1999-12-20
PRIOR FILLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILLING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 34
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US-09-904-920A-34
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-903-603A-34
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APPLICANT:
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                 APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
   CURRENT
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APPLICATION NUMBER: US/09/904,920A
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Grimaldi, Christopher
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Gerritsen, Mary E.
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Botstein, David
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Stewart, Timothy A.
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Mather, Jennie P.
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Eaton, Dan L.
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ilarity 31.6%;
Conservative 3
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                                                                                                                                                   Nicholas F.
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; Pred. No. 1.6e-13;
36; Mismatches 85;
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                                       US-09-909-064-34
                                                            RESULT 14
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SEQ ID NO 34
LENGTH: 915
TYPE: PRT
Sequence 34, Application US/09909064 Patent No. 6818449
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
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FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US00/00219
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FILING DATE: 1999-12-20
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APPLICATION NUMBER: PCT/US99/30095
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APPLICATION NUMBER: PCT/US99/28564
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APPLICATION NUMBER: PCT/US99/28214
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APPLICATION NUMBER: PCT/US99/21090
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                                                                                                                    219 VANFSQIETLTSVFOK 234
                                                                                                                                                         191 --HFVDVDDLHIIVQE 204
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                                                                                                                                                                                                                                                                             99 LQYGSTVKNEFSLKTFKRKSEVERAVKRMRHLSTGTMTGLAIQYALNIAFSEAEGARPLR
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                                                                                                                                                                                                                                                                                                            76 VHVGSRPYTEFPFGQHSSGEAAQDAVRASAQRMGDTHTGLALVYAKEQLFAEASGARP--
                                                                                                                                                                                                                                                                                                                                                                                             16 ALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASL
                                                                                                                                                                                                                                                                                                                                                                                                                                           62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NOS: 423
                                                                                                                                                                                              ENVPRVIMIVTDGRPQDSVAEVAAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFL
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Pred. No. 1.6e
36; Mismatches
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GENERAL INFORMATION:

APPLICANT: Genentech, APPLICANT: Ashkenazi APPLICANT: Botstein,

Inc.

APPLICANT:

Ashkenazi, Avi Botstein, David Desnoyers, Luc Eaton, Dan L.

APPLICANT:

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US-09-909-064-34
                                                                                    Query Match
Best Local (
                                                                                                                                                                                                            SEQ ID NO 34
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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PRIOR FILING DATE: 2000-02-2
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
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CURRENT APPLICATION NUMBER: US/09/909,064
CURRENT FILING DATE: 2001-07-18
CURRENT FILING DATE: 7001-07-18
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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TYPE: PRT
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                                                                                                                                                       ORGANISM: Homo sapiens
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APPLICATION NUMBER: PCT/US99/23089
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                                16 ALARSGAERGPPASAPRGDLMFLLDSSASVSHYEFSRVREFVGQLVAPLPLGTGALRASL
                                                                  Similarity 62; Conserv
Kljavin, Ivar J
Mather, Jennie P
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher
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                                                                      Conservative
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art, Timothy A.
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f, Ellen
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                                                                                    11.8%;
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                                                                  Score 253.5;
Pred. No. 1.6e
36; Mismatches
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                                                                  1.6e-13;
ches 85;
                                                                                                     DB 2;
                                                                                                     Length 915;
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RESULT 15
US-09-905-381A-34
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PRIOR FILING DATE: 2000-02-22
PRIOR PELING DATE: 2000-02-22
PRIOR PELING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR PILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/2094
PRIOR APPLICATION NUMBER: PCT/US99/2094
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,381A
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PRIOR FILING DATE: 1999-11-29
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PRIOR APPLICATION NUMBER: PCT
PRIOR FILING DATE: 1999-10-05
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PRIOR APPLICATION NUMBER: PCT/US99/21547
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                                  APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
APPLICATION NUMBER: PCT/US99/28564 FILING DATE: 1999-12-02
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o. 6818746
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher J.
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Gerritsen, Mary E
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Filvaroff, Ellen
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Eaton, Dan L.
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Botstein, David
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Mather, Jennie P.
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; PRIOR APPLICATION NUMBER: PCT/US99/28565; PRIOR FILING DATE: 1999-12-02; PRIOR APPLICATION NUMBER: PCT/US99/30095; PRIOR APPLICATION NUMBER: PCT/US99/30091; PRIOR FILING DATE: 1999-12-20; PRIOR APPLICATION NUMBER: PCT/US99/30991; PRIOR FILING DATE: 1999-12-20; PRIOR APPLICATION NUMBER: PCT/US99/30999; PRIOR FILING DATE: 1999-12-20; PRIOR FILING DATE: 1999-12-20; PRIOR FILING DATE: 1909-10-20; PRIOR FILING DATE: 2000-01-05; NUMBER OF SEQ ID NOS: 423; SEQ ID NO 34; LENGTH: 915; TYPE: PRT ORGANISM: Homo sapiens
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Search completed: February 13, 2006, 07:50:52 Job time: 65.3077 secs
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219 VANFSQIETLTSVFQK 234
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Result
No.
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-MODEL-frame+ n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10699035/runat_13022006_062447_25513/app_query.fasta_1
-Q=/abss/ABSSWEB_spool/US10699035/runat_13022006_062447_25513/app_query.fasta_1
-DB=Issued_Patents_AA_-OpmT=fastan_-SUFFIX=rai_-MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Dits_START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR_SCORE=pct_-THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL_-OUTFMT=pto -NORM=ext_-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-HOST=abss02p_-USER=US10699035_@CGN 1 1 101 @runat 13022006_062447_25513
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS-10 -XGAPDF=10 -XGAPDF=6
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Maximum DB
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/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-09-252-991A-20375

US-09-252-991A-20375

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APPLICANT: Dumas Milne Edwards, J.B.
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ALIGNMENTS

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Percent Similarity:
Best Local Similarit
Query Match:
DB:
                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 6277
LENGTH: 77
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-699-035A-5 (1-1254) x US-09-513-999C-6277
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APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and
Patent No. 6783961
                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 59.US2.REG
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LOCATION: 66
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                              1.61e-18
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LENGTH: 860
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEO ID NOS: 33142
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TITLE OF INVENTION: ABSULINGAN FOR DIAGNOSTICS AND THERAPEUTICS FILE REPRESENCE: 107162.10 (8707/25.991A)	8-991A-30843 10-30843, Application US/09252991A 10-	Db 640 gAlaAlaAlaBroArgAlaGlyArgGlyLeuArgGlyAsp 654
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LENGTH: 511
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25101
LENGTH: 917
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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GENERAL INFORMATION:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABBUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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                                                                                                                                     CACCGCCTACCTGGTGACCGTGACCGCCGT----CCGCTCGGGCCGCGAGAGCGCGCT 1160
                                                                                                                                                                       ValArgGlyGlyGlyArgSerAlaProAlaIleArgArgArgSerGlyAlaGlyGlnAsp
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DB:
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Best Local Similarity:
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20375
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   GluGlyGlyHisArgArgProAspGlyAspArgGluArgArgLeuArgArgValGlnArg
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Best Local Si
Query Match:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NO 31790
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RESULT 10
US-09-252-991A-31760
; Sequence 31760, Applic
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: MARC J.
; TITLE OF INVENTION:
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US-09-252-991A-30843 (Sequence 30843, Application US/09252991A) ; Sequence 30843, Application US/09252991A ; Sequence 30843, Application US/09252991A ; Patent No. 6551795 ; GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield et al. ; APPLICANT: Marc J. Rubenfield et al. ; TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS ; FILE REFERENCE: 107196.136 ; CURRENT APPLICATION NUMBER: US/09/252,991A ; CURRENT FILING DATE: 1999-02-18 ; PRIOR APPLICATION NUMBER: US 60/074,788 ; PRIOR FILING DATE: 1998-02-18	Oy 163 CCGGAACCCGGGAGAACTCGTAGTGAGAGACGCTGGCTGAGCTGTCCAGCAGCAGCACATCA 104		Db 326 ProAspAlaLeubroArgLeuAlaGlyLysProGlyArgTyrProAlaGluPheAla 344 Qy 436 CGCATCTGTCACCCACCACCACCACTTTGGCACCCTGGCCGGCACCTGATGCTTCAG 377	Oy 682 GGAAGCCGCTGGACGTGATCTCCGTGGCATGGAGCT 647

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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30843
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27068

LENGTH: 638

TYPE: NET
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ENERAL INFORMATION:
APPLICANT: Marc J.
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ORGANISM: Pseudomonas aeruginosa
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SOFTWARE: PatentIn version 3.0 SEQ ID NO 57 LENGTH: 755
                                                                                                                                                Sequence 57, Application US/09919497
Patent No. 6773883
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION
FILE REFERENCE: B0801/7225
                                                     CURRENT APPLICATION NUMBER: US/09/919,497 CURRENT FILING DATE: 2001-07-31 PRIOR APPLICATION NUMBER: US 60/221,735 PRIOR FILING DATE: 2000-07-31 NUMBER OF SEQ ID NOS: 100
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                                                                                                                                                                Sequence 18035, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO FITTLE OF INVENTION: AERUGINSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18035
LENGTH: 783
              Best Local Similarity:
Query Match:
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US-09-252-991A-18035
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                                                                                                                                                                     Query Match:
                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19127
LENGTH: 590
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19127, Appl. Patent No. 6551795
GENERAL INFORMATION:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
FILE REFERENCE: 107196.136
CURRENT FILLING DATE: 199-02-18
CURRENT FILLING DATE: 199-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
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